

GenCore version 5.1.6
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M nucleic - nucleic search, using sw model

run on: October 22, 2003, 07:27:11 ; Search time 5513 Seconds
(without alignments)
11197.647 Million cell updates/sec

title: US-10-006-852-1

perfect score: 1509
sequence: 1 agggcgctctccacgcgcgt.....agaagcgtggtatctgctaa 1509

scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

searched: 2888711 seqs, 20454813386 residues

total number of hits satisfying chosen parameters: 5777422

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

GenEmbl.*

1: gb.ba.*

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4: gb.om.*

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6: gb.pat.*

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37: em.sv.*

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39: em.htgo.mus.*

40: em.htgo.other.*

41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1509	100.0	1509	8 ATU10034	U10034 Arabidopsis
2	1507.4	99.9	1509	6 AX507115	AX507115 Sequence
3	1507.4	99.9	1509	6 AX651552	AX651552 Sequence
4	1507.4	99.9	1509	8 BT001047	BT001047 Arabidops
5	1507.4	99.9	1813	8 AF094464	AF094464 Arabidops
6	907.4	60.1	1776	8 AF353615	AF353615 Nicotiana
7	883.4	58.5	1705	8 AF020425	AF020425 Nicotiana
8	881.8	58.4	1785	8 PETGADX	L16797 Petunia hyb
9	881.8	58.4	1785	8 PETGLUDSCA	L16977 Petunia hyb
10	881.8	58.4	1929	8 NTU54774	U54774 Nicotiana t
11	877	58.1	1672	8 AF352732	AF352732 Nicotiana
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21	854.2	56.6	1482	6 AX506242	AX506242 Sequence
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41	393	26.0	5160	6 AX461514	AX461514 Sequence
42	393	26.0	81490	8 F12P19	AC009513 Sequence
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ALIGNMENTS

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LOCUS	Arabidopsis thaliana	Columbia	glutamate decarboxylase (GAD) mRNA,		
DEFINITION	complete cds.				
ACCESSION	U10034				
VERSION	U10034.1	GI:497978			
KEYWORDS	Arabidopsis thaliana				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;				
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi				
REFERENCE	1 (bases 1 to 1509)				
AUTHORS	Arazi,T., Baum,G., Snedden,W.A., Shelp,B.J. and Fromm,H.				

TITLE Molecular and biochemical analysis of calmodulin interactions with the calmodulin-binding domain of plant glutamate decarboxylase
JOURNAL Plant Physiol. 108 (2), 551-561 (1995)
MEDLINE 95334488
PUBMED 7610159
REFERENCE 2 (bases 1 to 1509)
AUTHORS Fromm, H.
Direct Submission
Submitted (25-MAY-1994) Hillel Fromm, Department of Plant Genetics, Weizmann Institute of Science, Rehovot 76100, Israel
Weizmann Location/Qualifiers

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IGIN

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1501 ATCTGCTAA 1509
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1501 ATCTGCTAA 1509

RESULT 2
AX507115
LOCUS
DEFINITION
AX507115
SESSION
AX507115.1 GI:23388352
BYWORDS
SOURCE
ORGANISM
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

REFERENCE
1
AUTHORS
TITLE
JOURNAL
Harper, J.F., Kreps, J., Wang, X. and Zhu, T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 1810 28-FEB-2002;
The Scripps Research Institute (US); Syngenta Participations AG
(CH)

FEATURES
source
Location/Qualifiers
1..1509
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432 a 322 c 385 g 370 t

BASE COUNT
432 a 322 c 385 g 370 t

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Best Local Similarity 99.9%; Score 1507.4; DB 6; Length 1509;
Matches 1508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DEFINITION
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AX651552 1509 bp DNA linear PAT 22-MAR-2003

CESSION AX651552
RSTON AX651552.1 GI:29154370
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ORGNISM Arabidopsis thaliana
Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
REFERENCE Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
AUTHORS Katagiri,P., Quan,S., Tao,Y., Whitham,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 0300898-A 360 03-JAN-2003;
SYNGENTA Participations AG (CH)
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IGIN

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Best Local Similarity 99.9%; Pred. No. 0;
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DEFINITION Arabidopsis thaliana
ACCESSION BT001047 GI:24111354
VERSION BT001047.1
KEYWORDS FLI CDNA.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1509)
REFERENCE Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
AUTHORS Chan,M.M., Chang,C.H., Dale,J.W., Hayashizaki,Y., Hsuan,V.W.,

TITLE
JOURNAL
REFERENCE
AUTHORS

Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu.G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.: Arabidopsis ORF clones unpublished Submitted (bases 1 to 1509)

Chen,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P., Chan,M.M., Chang,C.H., Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M., Southwick,A., Tang,C.C., Toriumi,M., Wallender,E.K., Wong,C., Wu,H.C., Yamada,K., Yu.G., Yuan,S., Shinozaki,K., Davis,R.W., Theologis,A. and Ecker,J.R.

TITLE
JOURNAL
COMMENT

Direct Submission Submitted (18-OCT-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-Length cDNA' : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.)

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Banh,J., Bowser,L., Chan,M.M., Chang,B., Dale,J.M., Goldsmith,A.D., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera,C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wu,H.C., Yamada,K., Yamamura,Y., Yu,G., Davis,R.W., Theologis,A. and Ecker,J.R.

Cheuk,R. (SSP/Salk) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES
source Location/Qualifiers

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BASE COUNT
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Query Match 99.9%; Score 1507.4; DB 8; Length 1509;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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CUS AY094464 1813 bp mRNA linear PLN 05-MAY-2002
FINITION Arabidopsis thaliana AT5g17330/MKP11_18 mRNA, complete cds.
CESSION AY094464
YWORDS AY094464.1 GI:20453186
URCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

PERENCE
AUTHORS Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Ban, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
Arabidopsis cDNA clones
Unpublished
2 (bases 1 to 1813)

TITLE
JOURNAL
PERENCE
AUTHORS Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Ban, J., Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A. and Ecker, J.R.
Direct Submission
Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory (SIGnAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-Length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Ban, J., Bowser, L., Chang, E., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Shinn, P. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES
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BASE COUNT 504 a 384 c 417 g 508 t
ORIGIN

Query Match 99.9%; Score 1507.4; DB 8; Length 1813;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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RESULT 6
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 AF353615
 VERSION
 AF353615.1
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 GI:13752461
 SOURCE
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 ORGANISM
 Nicotiana tabacum
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 1 (bases 1 to 1776)
 Yevtushenko,D., McLean,M.D., Peiris,S.E., Van Cauwenberghe,O.R. and Shelp,B.J.
 AUTHORS
 Two isoforms of tobacco glutamate decarboxylase are regulated by calcium/calmodulin and differ in organ distribution
 TITLE
 Unpublished
 JOURNAL
 2 (bases 1 to 1776)
 McLean,M.D., Yevtushenko,D. and Shelp,B.J.
 REFERENCE
 Direct Submission
 AUTHORS
 Submitted (26-FEB-2001) Department of Plant Agriculture, University of Guelph, Division of Biotechnology, Bovey Building, Guelph, Ontario N1G 2W1, Canada
 JOURNAL
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1321 ATGCTGAGCTCGATGAGCTTCTTCTGAGAGTGAATTCACAAAATA 1365
1409 CTCACGAGCTGGACACTTCCAGCTTAGGCTGAGCGCCAAATTA 1453

RESULT 7

AF020425

LOCUS

DEFINITION

AF020425

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

REFERENCE

FEATURES

source

gene

CDS

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches 1125;

Conservative

0;

Mismatches

351;

Indels

21;

Gaps

1;

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

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Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

AF020425

Nicotiana tabacum glutamate decarboxylase isozyme 1 (NtGAD1) mRNA,

complete cds.

AF020425

AF020425.1

GI:3252855

Nicotiana tabacum (common tobacco)

Nicotiana tabacum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.

1 (bases 1 to 1705)

Yun,S.J. and Oh,S.H.

Cloning and characterization of a tobacco cDNA encoding

calcium/calmodulin-dependent glutamate decarboxylase

Unpublished

2 (bases 1 to 1705)

Yun,S.J.

Direct Submission

Submitted (21-AUG-1997)

Faculty of Biological Resources Science,

Chonbuk National University, 664-14 1-ga Tokjin-dong, Chonju,

Chonbuk 561-756, South Korea

Location/Qualifiers

1. .1705

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1. .1705

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71. .1561

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BASE COUNT 523 a 301 c 385 g 496 t

Query Match 58.5%; Score 883.4; DB 8; Length 1705;

Best Local Similarity 75.2%; Pred. No. 7.9e-247;

Matches 1125; Conservative 0; Mismatches 351; Indels 21; Gaps 1;

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Qy 61 CGTTACGTCCGTACTTCACTTCTAGGTTCAAGATCGCGGAAAACTCGATTCTAAGGAA 120

Db 131 CGATAGTTCGTACTTCTTCCGAGGTTTAGATCCAGAGATTCGATACCAAGGAA 190

Qy 121 GCGCGGTATCAGATCATCAACGACGAGCTGATGCTTTGACGGGAAATCCACGGTTGAACCTTA 180

Db 191 GCAGCATATCAAAATCAAAATGATGAGCTTATGTTAGATGGAATCCAAAGACTAAATTTA 250

Qy 181 GCCTCCTTTGTGACGACATGATGGAGCTGAGGTGATGAATAAATCATCATGCTCCCTCAATC 240

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RESULT 8
PETGAD
LOCUS Petunia hybrida glutamate decarboxylase (gad) mRNA, complete cds.
DEFINITION
ACCESSION L16797
VERSION L16797.1 GI:294111
KEYWORDS glutamate decarboxylase.
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 1785)
Baum, G., Chen, Y., Arazi, T., Takatsui, H. and Fromm, H.
A plant glutamate decarboxylase containing a calmodulin binding
domain. Cloning, sequence, and functional analysis
J. Biol. Chem. 268 (26), 19610-19617 (1993)
J. Biol. Chem. 268 (26), 19610-19617 (1993)
8366104
COMMENT Original
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BASE COUNT 550 a 298 c 401 g 536 t
ORIGIN
Query Match 58.4%; Score 881.8; DB 8; Length 1785;
Best Local Similarity 74.9%; Pred. No. 2.3e-246;
Matches 1121; Conservative 0; Mismatches 367; Indels 9; Gaps 1;
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732 GTTAAAGCTTGAATGATCTTTGTTGCGAAGAAACAAAGAAACCGGATGGGATACACCA 791
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RESULT 9

PETGLUDECA

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

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BASE COUNT 550 a 298 c 401 g 536 t

ORIGIN

Query Match 58.4%; Score 881.8; DB 8; Length 1785;

Best Local Similarity 74.9%; Pred. No. 2.3e-246;

Matches 1121; Conservative 0; Mismatches 367; Indels 9; Gaps 1;

Qy 1 ATGCTGCTCTCCCAAGCGGATTCGGAGTCGGAGTCCTCGTCCACTCCACATTCGCATCA 60

Db 72 ATGTTCTATCAAGACAGTGTCCGAGCGATGTGTCCATTCACCTCCAGTTGTTCTT 131

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RESULT 10
 NTU54774
 LOCUS
 DEFINITION
 Nicotiana tabacum glutamate decarboxylase (NtGAD1) mRNA, complete cds.
 ACCESSION
 U54774
 VERSION
 U54774.1
 GI:1777920
 KEYWORDS
 Nicotiana tabacum (common tobacco)
 Nicotiana tabacum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
 REFERENCE
 1 (bases 1 to 1929)
 Dharmasiri,M.A.N., Lu,Y.T. and Harrington,H.M.
 Cloning and sequencing of a tobacco cDNA encoding glutamate decarboxylase
 Unpublished
 2 (bases 1 to 1929)
 Dharmasiri,M.A.N., Lu,Y.T. and Harrington,H.M.
 Direct Submission
 Submitted (11-APR-1996) M.A. Nihal Dharmasiri, Plant Molecular Physiology, University of Hawaii, 3190 Maile Way, Honolulu, HI 96822, USA
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RESULT 11
AF352732 LOCUS 1672 bp mRNA linear PLN 02-MAY-2003
DEFINITION Nicotiana tabacum glutamate decarboxylase isozyme 1 mRNA, complete cds.
ACCESSION AF352732
VERSION AF352732.1 GI:13310812
KEYWORDS .
SOURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
Asteridales; Lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1672)
REFERENCE Yevtushenko,D., McLean,M.D., Peiris,S.E., Van Cauwenberghe,O.R. and
AUTHORS Shelp,B.J.
TITLE Two isoforms of tobacco glutamate decarboxylase are regulated by
calcium/calmodulin and differ in organ distribution
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1672)
AUTHORS Yevtushenko,D., McLean,M.D. and Shelp,B.J.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-2001) Department of Plant Agriculture, University
of Guelph, Division of Biotechnology, Guelph, Ontario N1G 2W1,
Canada
FEATURES
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VERSION    AY124873.1 GI:21700916
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SOURCE     Arabidopsis thaliana (thale cress)
ORGANISM  Arabidopsis thaliana
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AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Banh,J., Bowser,L.,
           Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
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           Lam,B., Lee,J.M., Lin,J., Miranda,M., Narusaka,M., Nguyen,M.,
           Onodera,C.S., Palm,C.J., Quach,H.L., Sakurai,T., Satou,M., Seki,M.,
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           and Ecker,J.R.
           Arabidopsis ORF clones
           Unpublished
REFERENCE  2 (bases 1 to 1485)
AUTHORS   Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Banh,J., Bowser,L.,
           Carninci,P., Chang,E., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
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Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W., Theologis, A., and Ecker, J.R.

TITLE

Submitted (17-JUN-2002) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y., and Shinozaki, K.

The Salk, Stanford, PGSC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L., Chan, M.M., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Jones, F., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

FEATURES

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FERENCE	1 (bases 1 to 1676)	
AUTHORS	Turano, F.J. and Fang, T.K.	
TITLE	Characterization of two glutamate decarboxylase cDNA clones from Arabidopsis	
JOURNAL	Plant Physiol. 117 (4), 1411-1421 (1998)	
MEDLINE	98369120	
PUBMED	9701597	
FERENCE	2 (bases 1 to 1676)	
AUTHORS	Turano, F.J. and Thakkar, S.	
TITLE	Direct Submission	
JOURNAL	Submitted (21-JAN-1996) Frank J. Turano, Climate Stress Lab, USDA/ARS, BARC-West, Bldg. 046A, Beltsville, MD 20705, USA	
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CDS	Arabidopsis thaliana glutamate decarboxylase (GAD2) mRNA, complete cds.	
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URCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	
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AUTHORS	1. (bases 1 to 1681)	
TITLE	Zik, M., Arazi, T., Snedden, W.A. and Fromm, H.	
JOURNAL	Two isoforms of glutamate decarboxylase in Arabidopsis are regulated by calcium/calmodulin and differ in organ distribution	
MEDLINE	Plant Mol. Biol. 37 (6), 967-975 (1998)	
PERENCE	98363649	
PUBMED	9700089	
FERENCE	2 (bases 1 to 1681)	
AUTHORS	Zik, M., Arazi, T. and Fromm, H.	
TITLE	Direct Submission	
JOURNAL	Submitted (25-FEB-1996) Hillel Fromm, Plant Genetics, Weizmann Institute of Science, Rehovot 76100, Israel	
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Direct Submission
Submitted (05-OCT-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J., Satou, M., Kaniya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGEN (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Cheuk, K., Chen, H., Kim, C.-J., Koesse, E., Meyers, M.C., Shinn, P., Bath, J., Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P. X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Nguyen, M., Onodera, C. S., Palm, C. J., Pham, P. K., Quach, H. L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.

Location/Qualifiers

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Copyright (c) 1993 - 2003 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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AUTHORS	Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.				
TITLE	Maize Mapping Project/Dupont Consensus Sequences for Design of Overgo Probes				
JOURNAL	Unpublished (2002)				
REFERENCE	2	(bases 1 to 1168)			
AUTHORS	Coe,E.H.				
TITLE	Direct Submission				
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA				
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the				

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AUTHORS    Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLE       A large scale analysis of cDNA in Arabidopsis thaliana: Generation
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MEDLINE    20363093
PUBMED     10907847
COMMENT     Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
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PUBMED
10307847
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
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DB      241 GTTCAACATCGTCTCAAGAGCAGGAGTGCACCTTGTGCGCTTTCTCCTTCAAGAGATAG 300
QY      1149 CAGCTGTCACTGAGTTCGAAATCTCCGACATGTTTCGACAGTATGATGATAGTATGCTC 1208
DB      301 CAGCTGTCACTGAGTTCGAAATCTCCGACATGTTTCGACAGTATGATGATAGTATGCTC 360
QY      1209 GGCCTACACAATGCCCTCCAAATGCAACAACATCACTGTTCTTCGTGTGGTTATCAGAGA 1268
DB      361 GGCCTACACAATGCCCTCCAAATGCAACAACATCACTGTTCTTCGTGTGGTTATCAGAGA 420
QY      1269 AGATTTCTCGAGAACACTCGCTGAGAGACTTCTGATCGATATAGAGAAAGTATCGTGA 1328
DB      421 AGATTTCTCGAGAACACTCGCTGAGAGACTTCTGATCGATATAGAGAAAGTATCGTGA 480
QY      1329 GCTCGATGAGTTCCTTCGAGAGTGAATTCACAAAATATCACTTGGACAGAGAGAGTGA 1388
DB      481 GCTCGATGAGTTCCTTCGAGAGTGAATTCACAAAATATCACTTGGACAGAGAGAGTGA 540
QY      1389 ATCTAACA 1396
DB      541 ATCTAACA 548

RESULT 4
CB655721
LOCUS
DEFINITION
OSUNEC09G09.f OSUNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC09G09 5', mRNA sequence.
CB655721
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 811)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
```

REFERENCE	Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry									
AUTHORS	D., Wood,T.C., Leslie,A. and Wilkins,T.A.									
TITLE	An integrated analysis of the genetics, development, and evolution of the cotton fiber									
JOURNAL	Unpublished									
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: TAATACGACTCACTATAGGG High quality sequence start: 2 High quality sequence stop: 718. Location/Qualifiers									
FEATURES	source									
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ORIGIN	Query Match 34.8%; Score 525.2; DB 10; Length 837; Best Local Similarity 78.9%; Pred. No. 1.3e-142; Matches 637; Conservative 0; Mismatches 169; Indels 1; Gaps 1;									
Qy	1	ATGGTGCTCTCCACGCGGATCGGAGTCGGAGTCGGAGTCCTCGGTCCACTCCACATTCGCAATCA	60							
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Db	92	CGTTATGTCGGAACCTCACTGCCAGGTTCCAAAATGCCAGAAAACCTCCATACCAAAAGAG	151							
Qy	121	GCGCAGTCACAGATCATCAACGACGAGCTCATGCTTGACGCGGAATCCACGGTTGAACCTTA	180							
Db	152	GCTGCTTATCAGATCATCAATGATGAACTCATGCTTGATGCAACCCAAAGTTGAACTT	211							
Qy	181	GCCTCCTTTGTGACGACATCGATGGAGCCCTCAGTGTGATAAACTCATCATGCTCCTCCATC	240							

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212 GCCTCTTTTGTACTACATGGAGGCTGAATGTGATAGCTTATAATGGACTCCATC 271
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241 AACAGAACTATGTTGACATGACGAGTACCCGCTCACCCGCACTTCAGAACCGATGT 300
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601 CAGAACACCACTTTGTTGCGGACATTTCTGGTTCCACTCTTAATGAGAAATTCGAAGAT 660
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632 GAAACACCACTGTGTAGCTGCAATCTTGGTTCAACCCCTCAATGAGAAATTTGAAGAT 691
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751 ATTCAATGTTGACGCTAGTGGTGGATTTATTCGGCCATTTTGTACCCAGAACTTGAG 810
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811 TGGGACTTCAAGGCTCCCTTGTGAAG 837
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EST611520 KVVC Medicago truncatula cDNA clone pKVVC-10G4, mRNA
sequence.
BQ165651
BQ165651.1 GI:20308272
EST.
Medicago truncatula (barrel medic)
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
1 (bases 1 to 819)
VandenBosch, K., Endre, G., Silverstein, K., Town, C.D., Van Aken, S.,
Utterback, T., Cheung, F. and Fraser, C.M.
The Medicago truncatula 'kiloclone' set; ESTs selected and
re-arrayed from various libraries
Unpublished
Contact: VandenBosch K
Department of Plant Biology
University of Minnesota
220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA
Tel: 612 624 2755
Fax: 612 625 1738
Email: kvandenb@chs.umn.edu
TIGR sequence name: MTNAJ76TK Alias Clone name: MHAM-5712 More
information is available at: www.medicago.org

Seq primer: SKmod (CTA gAA CTA gtg gAT cc).
Location/Qualifiers
1. .819
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/clone_lib="KVVC"
/note="Vector: pBluescript SK-; Site1: EcoRI; Site 2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
BASE COUNT 245 a 158 c 188 g 228 t
ORIGIN
Query Match 34.3%; Score 517.4; DB 13; Length 819;
Best Local Similarity 79.4%; Pred. No. 2.4e-140; Indels 1; Gaps 1;
Matches 625; Conservative 0; Mismatches 161;
QY 3 GGTGCTCTCCACGCGGTATCGGAGTCGGAGCTCTCCGTCCACTCCACATTCGCATCAG 62
DB 31 GGTCTCTCAAGACAGCCTCGAGTCTGATGCTCTGTCCACTCAACCTTTGCTTCTCG 90
QY 63 TTACGTCCTGACTTCACTTCTTAGGTTCAAGATGCGGAAACTCGATTCCTAAGAGAGC 122
DB 91 CTATGTCAGAACTTCACTTCTTAGATTTCAAGATGCGGAGGAGTCTATACCAAGAGATG 150
QY 123 GCGGTATCAGATCATCAACGACGAGCTGATGCTTCAAGGGAATCCAGGTTGAACTTAGC 182
DB 151 AGCATACCAATATATTAACGATGAATGATGCTTATGGAACCCCTAGATTGAAATTTGGC 210
QY 183 CTCCTTTGTGACGACATGATGAGCTGAGTGTGATAAACTCATCATGCTCTCCATCAA 242
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DB 271 CAAGAACTAGTTGACATGAGTGAATACCCAGTCCACTGAGCTACAGATCGGTGTGT 330
QY 303 GAACATGATTGACATCTATTCAATGACCCGTTAGAAAGGCGGAGACCGCGCTCGGAGT 362
DB 331 TAACATGATAGCTCATCTTTTCAATGACCACTTGAAGAGATGAGGCTGCAGTTGGTGT 390
QY 363 AGGAACCGTTGGATCATCGGAGCCCATATGTTGGCGGTTTGGCGCTTCAAGCGTAAATG 422
DB 391 TGGCACTGTTGGCTCATCAGAGGCTATATGTTAGCTGGATTGGCATTCAAAAGGAAGTG 450
QY 423 GCAGAAACAAAGCGCAAGCTGAAGGCAAAACCGCTCGATAAACCAACATTTGCACCGAGC 482
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QY 662 TTAACCTTTGAACGATCTCTTGGTGTAAAGAAACAAAGAAACCGGATGGGATACACCAA 721
DB 691 TTAACGCTTAAACGATCTCTTGGTGTAAAGAAATTAAGGAAACTGATGGGACACTCTCTA 750


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782 GGGACTT 788
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811 GGGATTT 817

SULT 7
040860
CUS
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OF12G05 OF Oryza sativa cDNA 5' similar to glutamate decarboxylase
1, mRNA sequence.
CESSION
RSION
YWORDS
URCE
ORGANISM      Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 821)
Bohnert,H.J.; Borchert,C.; Brazille,S.; Brooks,J.; Eaton,M.; Ferrea
,H.; Kawasaki,S.; McCollough,A.; Michalowski,C.B.; Palacio,C.;
Scara,G.; Wheeler,M. and Zepeda,G.R.
Functional Genomics of Plant Stress Tolerance
Unpublished
Contact: Michalowski,C.B.
University of Arizona
Bio Sciences West room 513, Tucson, AZ 85721, USA
Tel: 520-621-7982
Fax: 520-621-1697
Email: cbm@u.arizona.edu
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185 a 231 c 254 g 149 t 2 others
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Best Local Similarity 78.0%; Pred. No. 6.3e-138;
Matches 613; Conservative 0; Mismatches 173; Indels 0; Gaps 0;
132 GATCATCAACGACGAGTGCCTTGACGGGAATCCAGGTGGACTAGCTCCTTGT 191
5 GAGGATCAACGACGAGTGCCTTGACGGCAACCCGGCGCTGAACCTCGCTGTCGT 64
192 GACGACATGGATGGAGCTGTGATAAACTCATCATGTCTCTCCATCAACAAGAACTA 251
65 CACCACTGGATGGAGCCGAGTGGACAGCTCATCAGGCTCCGTCAACAAGAACTA 124
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125 CGTCACATGGACGAGTACCCCGTCACCAACCGAGCTCCAGAACCGATGTGTGAACATGAT 184
312 TGCATCATTTTCATGACCGTTAGAGAGCGGAGACCCCGCTCGAGTAGGAACCGT 371
185 TGCACACCTCTTTCAATGCTCTCTAGGGGACTCTGAAACCGCCCGGAGTCGGCACTGT 244
372 TGGATCATCGGAGGCCATAATTTGGCCGGTTTGGCCCTTCAAGCGTAAATGGCAGAACAA 431
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492 AGTGTGTTGGGAGAAATTGCTAGGTACTTTGAGTTGAACTTAAGGAAGTGAATTTGAG 551
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365 AGTTTGTCTGGGAGAAATTGCGCGGATCTTCGAGGTTGAGCTCAAGGAAGTGAAGCTGAG 424
552 TGAAGGATACATATGTGATGGACCCCTCAACAAGCTCTTGATATGGTTGATGAGAACACCAT 611
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425 TGACGGCTACTACGTCATGGACCCAGCTTAAGCCCGTGGATATGCTCGACGAGAACACCAT 484
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485 CTGCGTTCGCGCGATCCTCGGTCGACGCTGAACGGGAGTTTCGAGGACGTGAAGCTGCT 544
672 GAACGATCTCTTGTGCGAAAAGAAACAAGAACCCGATGGGATACCAATCCACGTGA 731
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792 ACTTCCCTTTGGTGAAGAGTATCAATGTGAGTGGTCAAGTATGAGACTTGTGTACCGAGG 851
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RESULT 8
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DEFINITION      CDNA clone RZ27f07R 5', mRNA sequence.
ACCESSION      AV552358
VERSION        AV552358.1 GI:8723771
KEYWORDS
SOURCE
ORGANISM      Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 554)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
20363093
PUBMED
10907847
COMMENT
Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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FEATURES
source
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/note=Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

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1 ATGTGCTCTCCACGCGGTATCGAGTCGACGCTCTCCGTCCTCCACTCCACATTCGCATCA 60
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 109 CGTTACGTCCTTCTTCACT 168
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 349 GTGAACATGATGACATCTATTCAATGACCGTTAGAGAGCGGAGACCGCGTCGGA 408
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 409 GTAGAACCGTTGGATCATCGAGGCCATATGTTGGCCGCTTTGGCCCTTCAAGCGTAAA 468
 421 TGGCAGACACGCGCAAGCTGAGGCAACCCGTCGATTAACCCACATGTCACCGGA 480
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BU026594 775 bp mRNA linear EST 23-AUG-2002
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 Clone OHG17F24, mRNA sequence.
 BU026594.1 GI:22462114
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 Helianthus annuus
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroidae;
 Heliantheae; Helianthus.
 1 (bases 1 to 775)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Bieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison,
 P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://compgenomics.ucdavis.edu/
 Unpublished
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742

FEATURES
 source

1..775
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 /note="Vector: pBRCDNASFIAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/
 TAG_LIB=OH_EFGHJ sunflower RHA280
 TAG_TISSUE=null
 TAG_SEQ=GCTAGTCGGG"

BASE COUNT 224 a 140 c 191 g 219 t 1 others
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Query Match 33.2%; Score 500.4; DB 13; Length 775;
 Best Local Similarity 77.8%; Pred. No. 2.3e-135; Matches 603; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
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 QY 421 TGGCAGAACACGCGCAAGCTGAGGCAACCCGTCGATTAACCCACATGTCACCGGA 480
 Db 61 TGGCAAAACAAAATGAAAGCTCTTGGCAAACTTGGGACAAACCTAAACATTTAAACCGG 120
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 QY 541 GTGAAATTCAGTCAAGGATCATGATGATGAGCCCTCAACAGCTGTTGATATGTTGAT 600
 Db 181 GTGAAGTTTCAAGTCAAGGATCATGATGATGAGCCCTCAACAGCTGTTGATATGTTGAT 240
 QY 601 GAGAACACATTTGTTGTCGACATCTTGGTTCACCTCTTAATGGAGAAATTCGAAGAT 660
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 QY 661 GTTAAACTCTCAACGATCTCTTGGTGAAAGAAACAAAGAAACCGGATGGATACACCA 720
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 Db 481 GTTTACCGGAAATTTGGTGGGTCAITTTGGAGGAACAAGATGACTTGCCTGATGAATC 540
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 Db 541 ATCTTTTCAATCAATATCTTGGTGTCTGATCAACCAACTTTTCACTCTCAACTTCTCCAAA 600

Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
 belongs to contig OH_CA_Contig2686, see http://cgpdb.ucdavis.edu/
 for details.
 Plate: OHG17 row: F column: 24.

961 GGTTCAGTCAAGTCATTGCTCAATCTACCAACTTATCCGATTTGGGCCACGAGGGTTAC 1020
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601 GGTTCTAGTCAAATAATTTGCTCAATCTATCAGTTTCATTGCTTGGGTTTCGAGGGATAC 660
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1021 AGAATATGTATGGAGATTGCAGAGAGAAATATGATCTCTTAAGGGAAGACATTGAGAG 1080
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661 AAGAGTATCATGGAAAACCTGNCAGAAAATGCAAAATGTTCTTAAGAAAGGTTTGGAGAAA 720
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1081 ACAGAAAGGTTCAACATCGTCTCAAGGACGAGGGAGTGCACATTGTCGCTTCTCT 1135
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721 ACCGGACGGTTCAACATCATCTCTAAAGAACACGGCGCTCCCACTTGTAGCTTCT 775
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SULT 10

813481

CUS

FINITION

CA48LN101F-E8 Cabernet Sauvignon Leaf - CA48LN Vitis vinifera cDNA

clone CA48LN101F-E8 5', mRNA sequence.

CA813481

CA813481.1 GI:26262418

EST.

Vitis vinifera

Vitis vinifera

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosids

; Vitaceae; Vitis.

1 (bases 1 to 786)

Goes da Silva, F., Lim, H., Iandolo, A., Baek, J., Jones, K., Walker

, M.A. and Cook, D.R.

Transcriptional responses of Vitis vinifera to infection by the

bacterial pathogen Xylella fastidiosa

Unpublished

Contact: Doug Cook

CAES Genome Facility

UC Davis Department of Plant Pathology

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Tel: 530 754 6561

Fax: 530 754 6617

Email: drcocook@ucdavis.edu

Seq primer: GTTATCAGTCGACGGTACC.

ATURES

source

1. 786

/organism="Vitis vinifera"

/moltype="mRNA"

/cultivar="Cabernet Sauvignon"

/db_xref="taxon:29760"

/clone="CA48LN101F-E8"

/sex="hermaphrodite"

/dev stage="Late season sample"

/lab_host="DMSalpha"

/clone_lib="Cabernet Sauvignon Leaf - CA48LN"

/note="Organ; Leaf; Vector: pDNR; Site: Sfil; Site.2:

Sfil; CA48LN is a cDNA library of Cabernet Sauvignon

leaves. The leaves were collected on September 20, 2001,

in Napa Valley, California, and represent leaves in late

season development. These leaves were asymptomatic and

verified to be non-infected with the bacterial pathogen,

Xylella fastidiosa, based on a diagnostic assay using PCR

and Xylella-specific primer pairs. cDNAs were made by

oligo-dT priming and directionally cloned. 5' and 3'

adaptors were used in cloning as follows:

5'-AAGCAGTGTATCAACGAGATGTCATACGCGCGG-3' and

5'-ATTCTAGAGCGCGCGCGGCGACATG-dT(30)NN-3'. Library was

constructed using the Clontech Creator SMART kit and

size-selected to contain the 0.5-3 kb size fraction."

SE COUNT 222 a 163 c 200 g 201 t

IGIN

Query Match

Best Local Similarity 32.9%; Score 496.6; DB 14; Length 786;

Matches 612; Conservative 0; Mismatches 174; Indels 1; Gaps 1;

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301 GGCCACACAGTACGGGCTTGTGTATGCTGGCATAGTTGGGTGATTTGGAGGAGTAAAGAG 360
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1003 TTGGGCCACGAGGTTTACAGAAATGTGATGGAGATTCGAGAGAAATATGATCTCTTA 1062
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481 TTGGGCCATGACGGGATATAGGAACTATTGGAAGAACTGTCAAGAAAAATGCAAGGGTGTCT 540
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RESULT 11

BQ971999

LOCUS

DEFINITION

QHB9G09.yg.ab1 QH ABCDI sunflower RHA801 Helianthus annuus cDNA

clone QHB9G09, mRNA sequence.

BQ971999

ACCESSION

VERSION

BQ971999.1 GI:22389520

KEYWORDS

SOURCE

EST.

Helianthus annuus (common sunflower)

Helianthus annuus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asterids; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.

1 (bases 1 to 762)

REFERENCE

AUTHORS

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison

BQ971999 762 bp mRNA linear EST 21-AUG-2002
QHB9G09.yg.ab1 QH ABCDI sunflower RHA801 Helianthus annuus cDNA
clone QHB9G09, mRNA sequence.

BQ971999
BQ971999.1 GI:22389520
EST.
Helianthus annuus (common sunflower)

Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asterids; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.
1 (bases 1 to 762)
REFERENCE
AUTHORS
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison

P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z., Church, S., Jackson, L., and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>
Unpublished
Contact: Alexander Kozik [R.W.Michelmores]
Department of Vegetable crops, R.W.Michelmores Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmores@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig2686, see <http://cgdb.ucdavis.edu/>
for details.
Plate: QHB9 row: G column: 09.

FEATURES

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/note="Vector: pBRCDNA51AB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformation made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at <http://cgdb.ucdavis.edu/>
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TAG TISSUE=hulls
TAG_SEQ=CGTAGTCGGG" 224 a 138 c 190 g 210 t

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Best Local Similarity 77.4%; Pred. No. 2.3e-131;
Matches 590; Conservative 0; Mismatches 172; Indels 0; Gaps 0;
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121 GCCAACGTTCCAGTTTGTGGAGAAATTTGTCGTATTTGAAGTGAGTTGAAGAA 180
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181 GTGAATGTGAGGAAGGTTACTACGTGTGATCTGTGAGAAAGCTGTGAGATGTTGAT 240
601 GAGAACACCATTTGTTGCGGACATTTCTGTTCCACTTTAATGAGAAATTCGAAGAT 660
241 GAAACACATTTTGTGTGCTCTATCTTGGTTCACCCCTCATGTTGAATTTGAAGAT 300
661 GTTAAACTCTGACATCTTGTGCGAAAGAACAAAGAACCGGATGGGATACACCA 720
301 GTTAAACGTTTAAATGACCTCTTGTGAGAAATTTGCAAGACCGGATGGGATACACCT 360
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361 ATTCAATGTGAGCGCTCAAGTGGAGTTTATGACCATTTATTTACCCGGAATTCGAA 420
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LOCUS HV_CBA0007K14f Hordeum vulgare seedling green leaf EST library
DEFINITION HVCDNA0004 (Blumeria challenged) Hordeum vulgare subsp. vulgare
cDNA clone HV_CBA0007K14f, mRNA sequence.
ACCESSION BF263784
VERSION BF263784.2 GI:13261070
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
Wing, R., Close, T.J., Klein, H., Wise, R., Wei, F., Begum, D.,
Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi,
D.W., Fenton, R.D., Oates, R. and Main, D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla13)
seedling leaf cDNA library
Unpublished
On Nov 17, 2000 this sequence version replaced gi:11194778.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 571
Seq primer: AATTAACCTCTCACTAAGG
High quality sequence stop: 721.
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/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
C.I. 16155 (Mla13) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate A27 (AvrMla13
of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;

FEATURES

source
1..823
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
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/db_xref="taxon:112509"
/clone="HV_CBA0007K14f"
/issue_type="seedling green leaf"
/lab_host="TJC121"
library HVCDNA0004 (Blumeria challenged)"
/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
C.I. 16155 (Mla13) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old
green seedlings were challenged with isolate A27 (AvrMla13
of Blumeria graminis f. sp. hordei, and leaves were
harvested 20 and 24 hr post-inoculation and snap frozen;

uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one cDNA library was made, and 1 million pfu were in vivo excised to give pluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinforfs A, Wise R (2001). Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgm/31/cover.html>)"

SE COUNT 209 a 187 c 249 g 175 t 3 others
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 VERSION BU025918.1 GI:22461438
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 REFERENCE 1 (bases 1 to 769)
 AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L., Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., Church,S., Jackson,L. and Bradford,K.
 TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
 JOURNAL http://compgenomics.ucdavis.edu/
 COMMENT Unpublished
 CONTACT: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
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 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akosik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig OH_CA_Contig2686, see <http://cgdb.ucdavis.edu/> for details.
 Plate: OHG12 row: C column: 07.
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 Best Local Similarity 77.7%; Pred. No. 2.6e-130;
 Matches 584; Conservative 0; Mismatches 168; Indels 0; Gaps 0;
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SULT 14
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clone QHf12C03, mRNA sequence.
BU023643
BU023643.1 GI:22459163
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Helianthus annuus (common sunflower)
Helianthus annuus
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Asteroideae;
Heliantheae; Helianthus.
1 (bases 1 to 750)
Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished
REFERENCE
AUTHORS
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Amundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig2686, see http://cgdb.ucdavis.edu/
for details.
Plate: QHf12 row: C column: 03.
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/clone_lib="QH_EFGHJ sunflower RHA280"
/note="Vector: pBRCDNA51AB; The library was constructed
from 11 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. cDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size bias. Details of each source of RNA and library
construction can be obtained at http://cgdb.ucdavis.edu/
TAG_SEQ=Not found"

BASE COUNT 221 a 132 c 187 g 210 t
ORIGIN

Query Match 32.0%; Score 482.8; DB 13; Length 750;
Best Local Similarity 77.7%; Pred. No. 3.4e-130;
Matches 593; Conservative 0; Mismatches 167; Indels 0; Gaps 0;
QY 361 GTAGAAACCGTTGGATCATCGGAGGCCATAATGTTGGCCGGTTTGGCCCTTCAAGCGTAAA 420
Db 1 GTTGAACCTGTGGCTCATCCGAGCCATCATGTTGGCCGGACTAGCTTTCAAAAGAAAA 60
QY 421 TGGCAGAACACGCGAAGCTGAAGCGCAACCCGTCGATAAACCCCAACATTTGTCAACCGA 480
Db 61 TGGCAAAACAAAATGAAAGCTCTTGGCAAAACCTTGGGACAAACCTTAACATTGTAACCGGG 120
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Db 541 ATCTTTTCATCACTAATCTTGTGTTGCTGATCAACCAACTTTTCACTCTCAACTCTTCCAAA 600
QY 961 GGTTCAGAGTCAAGTCAATGCTCAATACTACCAACTTATCCGATTGGGCCACGAGGGTTAC 1020

Sequence 30, Appl
Sequence 30, Appl
Sequence 443, App
Sequence 7, Appli
Sequence 20, Appl
Sequence 9, Appli
Sequence 21, Appl
Sequence 5, Appli
Sequence 4639, Ap
Sequence 1, Appli

Sequence 920, App
Sequence 783, App
Sequence 922, App
Sequence 3588, App

Sequence 1, Appl
Sequence 1480, Ap
Sequence 7302, Ap

Sequence 28, Appl
Sequence 73, Appl
Sequence 31, Appl

Sequence 187, App
Sequence 857, App

Sequence 15, Appl
Sequence 58, Appl
Sequence 61, Appl

See, e.g.,

duction

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ch 1509;
s 0; Gaps 0;
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CCACATTGCATCA 60
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CGATTCTAAGGAA 120

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Sequence 777, App
Sequence 30, Appl
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Sequence 7, Appl
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Sequence 9, Appl
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Sequence 610, App
Sequence 783, App
Sequence 922, App
Sequence 3388, App
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Sequence 1480, App
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Sequence 13198, App
Sequence 28, Appl
Sequence 73, Appl
Sequence 31, Appl
Sequence 132, App
Sequence 187, App
Sequence 857, App
Sequence 15, Appl
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Sequence 58, Appl
Sequence 61, Appl
Sequence 79, Appl

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Db	1261	ATCAGAGAAGATTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG	1320
Qy	1321	ATCGTGAGCTCGATGAGCTTCCTTCGAGAGTGATTCAAAAATATCACTTGGACAAGAG	1380
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Qy	1381	AGAGTGAATCTTAACAGCGATAACTTGATGGTCAACGGTGAAGAGACGATATCGACAAG	1440
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Db	1501	ATCTGCTAA	1509

RESULT 2
 US-09-938-842A-1810
 ; Sequence 1810, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Krepes, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRIPI300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1810
 ; LENGTH: 1509
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1810

Query Match	99.9%;	Score	1507.4;	DB	10;	Length	1509;
Best Local Similarity	99.9%;	Pred. No.	0;				
Matches	1508;	Conservative	0;	Mismatches	1;	Indels	0;
Gaps	0;						
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DB	1	ATGTGCTCTCCCA	CGCGGTATCGGAGTCGGAGCTCTCCGTC	CACTCCGATTCGCATCA	60		
QY	61	CGTTACGTCGTACTT	CACCTTCCTAGGTTCAAGNTGCGGAAAACTCGATTCCTTAAGAA	120			
DB	61	CGTTACGTCGTACTT	CACCTTCCTAGGTTCAAGATGCGGAAAACTCGATTCCTTAAGAA	120			
QY	121	CGCGCGTATCAGATCAT	CAACGACGAGCTGATGTTGACGGGAATCCACGTTTGAACTTA	180			
DB	121	CGCGCGTATCAGATCAT	CAACGACGAGCTGATGTTGACGGGAATCCACGTTTGAACTTA	180			
QY	181	GCCTCTTTTGTGACAT	GGATGGAGCGCTGAGTGTGATAAATCATCATGTCTCTCCATC	240			
DB	181	GCCTCTTTTGTGACAT	GGATGGAGCGCTGAGTGTGATAAATCATCATGTCTCTCCATC	240			
QY	241	AACAAGAACTATGTTG	CATGGACGAGTACCCCGTCCACCGAACTTCAGAACC	300			
DB	241	AACAAGAACTATGTTG	CATGGACGAGTACCCCGTCCACCGAACTTCAGAACC	300			

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Db 1381 AAGAGTGAATCTAAAGCGATACCTTGTGATGGTCAAGTGAAGAGCGGATATCGCAAG 1440
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 Db 1441 CAGAGAGATATCATCTACCTGGTGGAAAGATTTGTGCGCGACAGGAAGAGAGAGTGGT 1500
 Qy 1501 ATCTGCTAA 1509
 Db 1501 ATCTGCTAA 1509
 RESULT 3
 US-10-006-852-11
 ; Sequence 11, Application US/10006852
 ; Publication No. US20030046732A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kinnersely, Alan M.
 ; APPLICANT: Turano, Frank J.
 ; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
 ; FILE REFERENCE: 7224-65
 ; CURRENT APPLICATION NUMBER: US/10/006,852
 ; CURRENT FILING DATE: 2002-07-01
 ; PRIOR APPLICATION NUMBER: US 60/246,367
 ; PRIOR FILING DATE: 2000-11-07
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 11
 ; LENGTH: 1705
 ; TYPE: DNA
 ; ORGANISM: Nicotiana tabacum
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (71)..(1558)
 ; OTHER INFORMATION:
 US-10-006-852-11
 Query Match 58.5%; Score 883.4; DB 14; Length 1705;
 Best Local Similarity 75.2%; Pred. No. 1.2e-281;
 Matches 1125; Conservative 0; Mismatches 351; Indels 21; Gaps 1;
 Qy 1 ATGTGCTCTCCACAGCGGTATCGGAGTGGAGCTCTCGTCCACTCCACATTTCGCATCA 60
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GENERAL INFORMATION:
; APPLICANT: Kimersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Petunia x hybrida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)..(1571)
; OTHER INFORMATION:
US-10-006-852-15

Query Match 58.4%; Score 881.8; DB 14; Length 1785;
Best Local Similarity 74.9%; Pred. No. 4.2e-281;
Matches 1121; Conservative 0; Mismatches 367; Indels 9; Gaps 1;
QY 1 ATGGTGCTCTCCACGCCGTATCGGAGTCGGAGCTCTCGTCCACTCCACATTCGCATCA 60
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Db 192 GCAGCATATCGATCATATAATGATGACTGATGATGGAACCCAGGCTGAACCTG 251
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Db 252 GCTTCTTTTGTACATGAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
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QY 541 GTGAAATGAGTGAAGGATATATGATGAGGAGCTTCAACAAAGCTGTTGATATGATGATGAT 600
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841 GTGTACGCGAGGATTTGGTGGTGGTATCTGAGAGAAACAAAGAGGATTTGCTGAGGAATC 900
912 GTCTATGCTGATTTGGTGGTGGTATCTGAGAGAAACAAAGAGGATTTGCTGAGGAATC 971
901 ATCTTCCATATCAATTTCTGGTGGTGGTATCTGAGAGAAACAAAGAGGATTTGCTGAGGAATC 960
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1152 ACAGAAAGTTCAACATGCTCTCAAGAGAAATTCGAGAGAAATTCGAGAGAAATTC 1211
1141 AAGAAATGTGATGAGAAATTCGAGAGAAATATGATCGTCTAAGGAAAGACTTGAAG 1200
1212 AAGAAATGTGATGAGAAATTCGAGAGAAATATGATCGTCTAAGGAAAGACTTGAAG 1271
1201 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1260
1272 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1331
1261 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1320
1332 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1391
1321 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1380
1392 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1451
1381 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1440
1452 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1502
1441 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1497
1503 ATAGTGGCGGCTACAACATGCTTCAAAATGCAACACATCACTGTTCTCTGTTGGTT 1559

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SULT 5
-10-006-852-3
Sequence 3, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kinnerseley, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.1
SEQ ID NO 3
LENGTH: 1665
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:

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; NAME/KEY: CDS
; LOCATION: (17)..(1498)
; OTHER INFORMATION:
US-10-006-852-3

Query Match
Best Local Similarity 57.7%; Score 870.2; DB 14; Length 1665;
Matches 1110; Conservative 0; Mismatches 348; Indels 21; Gaps 1;

QY 31 GACGTCCTCCGTCACATTCACATTCGATCAGCTTACGTCGCTACTTCTCTAGGTTTC 90
DB 44 GATGAATCTCTCTGCAACATGTTCCGATCTCGATATGTTTCCGACTACATTCCTCAAGTAT 103
QY 91 AAGATGCGGAAACATCGATTCCTTAAGGAGCGGCTATCAGATCATCAACACGAGCTG 150
DB 104 GAGATTGGTGAGAAATTCGATTCGAAAGAGCGTGCATATCAGATCATAAAGATGAGCTG 163
QY 151 ATGCTTCAACCGGAAATTCACGCTTGAACCTTAGGCTCTTTGTGACGATGATGAGCTT 210
DB 164 ATGCTTCAACCGGAAATTCACGCTTGAACCTTAGGCTCTTTGTGACGATGATGAGCTT 223
QY 211 GAGTGTGATAAATCTCATCTGCTCTCCATCAACAGAACTATGTTGACATGACGAGTAC 270
DB 224 GAGTGTGATAAATCTCATCTGCTCTCCATCAACAGAACTATGTTGACATGATGAGTAC 283
QY 271 CCGCTCAACCGGAAATTCAGAAACCGATGTGAAACATGATGACATCTATTCAATGCA 330
DB 284 CCGCTCAACCGGAAATTCAGAAACCGATGTGAAACATGATGACATCTATTCAATGCA 343
QY 331 CCGTTAGAAAGGCGGAGACCGCGTTCGAGATGAGAAACCGTTGGATCATCGGAGGCCATA 390
DB 344 CCACTCAGGAAATCTCAGACGCGGCTGAGGAGTGGGACAGTTGGTTCTTCAGAAAGCATT 403
QY 391 ATGTTGCGCGGCTTGGCGCTTCAAGCGCTTAAATGCGAGAAACAAAGCGCAAGCTCAAGGCAA 450
DB 404 ATGTTGCGCGGCTTGGCGCTTCAAGCGCTTAAATGCGAGAAACAAAGCGCAAGCTCAAGGCAA 463
QY 451 CCGCTCAACCGGAAATTCAGAAACCGATGTGAAACATGATGACATCTATTCAATGCA 510
DB 464 CCGTTAGAAAGGCGGAGACCGCGTTCGAGATGAGAAACCGTTGGATCATCGGAGGCCATA 523
QY 511 GCTAGTACTTTGAGGTTGAACTTAAAGGAGTGAATTCAGTGAAGGATATCTATGTATG 570
DB 524 GCTCGGTACTTTGAGGTTGAACTTAAAGGAGTGAATTCAGTGAAGGATATCTATGTATG 583
QY 571 GACCTCAACAGGCTTTGATATGTTGATGAGAAACCAATGTTGTTGCGGACATTTCTT 630
DB 584 GATCCAGACAAAGCAGCAGAAATGGTAGACGAGAAACCAATCTGTGTGCGAGCCATATTG 643
QY 631 GGTTCACATCTTAATGGAGAAATTCGAGATGTTAAACTCTTGAACGATCTTGTGTCGAA 690
DB 644 GGTTCACATCTTAATGGAGAAATTCGAGATGTTAAACTCTTGAACGATCTTGTGTCGAA 703
QY 691 AAGAAACAAAGGAGGAGTGGGATACCAACATCCAGTGGATGCGGCAAGTGGAGATTC 750
DB 704 AAAAAACGAGGAGACTGTTTGAACACACCCGATCCAGTGGATGCGAGCAAGTGGAGGTTTC 763
QY 751 ATTGCACCGTTTGTATTCGGAATTCGGAATTCGGAATTCGGAATTCGGAATTCGGAATTC 810
DB 764 ATAGTCCGCTTTATCTATCTGAAATTCGGAATTCGGAATTCGGAATTCGGAATTCGGAATTC 823
QY 811 ATCAATGTGAGTGGTCAAGATTCGACTTGTGTACGCGAGGATTCGTTGGTGTGATCTGG 870
DB 824 ATCAATGTGAGTGGTCAAGATTCGACTTGTGTACGCGAGGATTCGTTGGTGTGATCTGG 883
QY 871 AGAAACAAAGAGGATTCGCTGAGGAACTCATCTTCCATATCAATTAATCTTGGTCTGAC 930
DB 884 AGGCGACGAGGATTTGCTGAGAGCTTATCTTTCATATTAAATTAATCTTGGTCTGAT 943
QY 931 CAACCCACCTTTTACTCTCAATTTCTCAAGGTTCAAGTCAAGTCAATGCTCAATCTACTAC 990
DB 944 CAACCCACCTTTTACTCTCAATTTCTCAAGGTTCAAGTCAAGTCAATGCTCAATCTACTAC 1003

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991 CAACCTATCCGATTCGGCCACGAGGTTTACAGAAATGTGATGGAGAATTGCAGAGAAAT 1050
1004 CAGCTCATCTGCTTGGATTCGAGGGGTACAAAATGTGATGGAGAATTGCATAGAGAAC 1063
1051 ATGATCGTCTTAAGGGAAGGACTTGAGAGAAGAGAAAGTTTCAACATCGTCTCAAGGAC 1110
1064 ATGGTGGTTCTCAAGAAAGGATAGAGAAAACAGAGCGTTTCAACATAGTCTCAAGGAC 1123
1111 GAGGAGTGGCACTTGTGCTTTCTCCTTGAAGATAGCACTGTACACTGAGTTCGAA 1170
1124 CAAGGAGTGCAGTGTAGCTTCTCTCAAGGACCATAGTTTCCAAACGAGTTCGAG 1183
1171 ATCTCGCATCTTCGCGAGTATGGATGGATAGTGC CGGCTACAAATGCCCTCCAAAT 1230
1184 ATCTCTGAGATCTAGCTCGTTTGGCTGGATCTCCAGCTTACATATGCTGCCGAT 1243
1231 GCACAACATCACTGTCTTCTGCTGGTATACAGAGAAGATTTCTCGAGAACACTCGCT 1290
1244 GCACAGCATCACGGTTCGCGTGTGTCTATCAGGGAAGATTTCTCAAGAACACTCGCG 1303
1291 GAGAGACTTGTGATCGATATAGAGAAAGTGTGCTGAGCTCGATGAGCTTCTTCGAGA 1350
1304 GAGAGACTTGTGCTGATATTCGAAGTGTCTCATGAGCTAGATACCTTGCCTTCCAAG 1363
1351 GTGATTCACAAATATCACTTGGACAAAGAGAGTGAATCTAAACAGCATTAACCTTGAT 1410
1364 AT-----ATCTAAGAGATGGGAATAGAAAGGATCGCGGAAAT 1402
1411 GTACGGTGAAGAGCGATATCGACAGCAGAGAGATATCATCACTGGCTGGAAGAAG 1470
1403 GTAAGGAGAGAAATGGAAGAGATTCGATGGAAATTTGTTGGATGGAGGAG 1462
1471 TTGTGCGCGACAGGAAGAGAGTGTGTCTCTAA 1509
1463 TTGTGAAGAGAGGAAGATGAATGTGTGTCTAA 1501

SULT 6

-10-005-602-1
Sequence 1, Application US/10005602
Publication No. US20030110530A1
GENERAL INFORMATION:
APPLICANT: Barry Shelp
APPLICANT: Alan Bown
TITLE OF INVENTION: TRANSGENIC PLANTS HAVING REDUCED
TITLE OF INVENTION: SUSCEPTIBILITY TO INVERTEBRATE PESTS
FILE REFERENCE: P84US3
CURRENT APPLICATION NUMBER: US/10/005,602
CURRENT FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1745
TYPE: DNA
ORGANISM: tobacco plant
-10-005-602-1

Query Match 57.3%; Score 864.2; DB 14; Length 1745;
Best Local Similarity 74.3%; Pred. No. 2.8e-275;
Matches 1113; Conservative 0; Mismatches 363; Indels 21; Gaps 1;
1 ATGGTGTCTCTCCACGCCGTATCGGAGTGGGACGTCTCGTCCACTCCACATTCGATCA 60
31 ATGGTCTGTCCAAGACAGCGTGGAAAGTGAAGTCTCATCCACTCCACTTTCGCTTC 90
61 GGTATCGTCGTAATTCATCTTCTAGTTCAAGATCGCGGAAAATCGATTCCTAAGAA 120
91 CGATATGTTCCAACTTCTCTTCCAGGTTAAAGATGCCAGAGATTTCAATACCAAGAA 150
121 GCGGCGTATCAGATCATCAACGAGCTGATGCTTGGCGGAATCCACGTTGAACTTA 180
151 GCAGCATATCAGATTAATATGATGAGCTTATGTATGATGGAAATCCAGGCTAAATTTA 210

181 GCCTCCTTTGTGACGACATGATGAGGCTTGAGTGTGATAAACTCATCTCTCTCCATC 240
211 GCATCTTTCTGTTTCAACATGATGAGCCAGAAATGTATAGCTTTAATGATGGATTCATT 270
241 AAACAAAGAACTATGTTGACATGAGCAGGATACCCCGTCAACCGAACTTCAGAACCGATG 300
271 AAACAAAGAACTACGTTGACATGAGTGAATACCCCTGTAACTCACTGAGCTTCAGAAATCGATGT 330
301 GTGAACATGATGACATCTATTCAATGACCGGTAGAAGGCGGAGAGCGCGTCCGGA 360
331 GTAAATATGATAGCTCATTTGTTTATGACACCATTTGGAGATGAGAGACTGCGAGTTGGA 390
361 GTAGAAACCGTTGGATCATTCGAGGCCATAATGTTGGCCGTTTGGCCTTCAACGCTAAA 420
391 GTTGAACCTGTTGGATCTCTGAAAGTATTATGCTTCTGGAATTAGCCTTTAAAGAGAA 450
421 TGGCAGAACAGCGGAAAGCTGAGGCGAAACCCGTCGATAAACCCAACTTGTCAACCGGA 480
451 TGGCAAAATAAAATGAAAGCCCAAGGCCAAGCCCTTTGATAGCCCAATATCGTCACCGGT 510
481 GCCAATGTTCAAGTGTGTGGAGAGAAATTCGCTAGGTACTTTGAGGTTGAACCTTAAAGGAA 540
511 GCTAATGCCAGTGTGTGGAGAGAAATTCGAAGGTATTTTGAAGTGGAGTTGAAGAA 570
541 GTGAATTTGAGTGAAGGATATCTATGTGATGGAACCTTCAACAGCTGTTGATGATGTTGAT 600
571 GTAAATTTGAGTGTGATCTATGTGATGGAACCTTGAAGAAAGCTGTGGAATGTTGGAT 630
601 GAGAACACCATTTGTTGTCGACATCTTCTGTTCCACTCTTAATGAGAAATTCGAAGAT 660
631 GAGATACCATTTGTTGTCGCTATCTTAGTTCAACACTCAATGTTGAATTTGAAGAT 690
661 GTTAACTCTTGAACGATCTCTTGTGCGAAAGAACAAAGAAACCGGATGGGATACACCA 720
691 GTTAAAGCGTTTGAATGACCTTTTGATTCGAAGAAACAAAGAAACCGGATGGGACACTCCA 750
721 ATCCACGTGATCGGCAAGTGGAGGATTCATGCAACCGTTTGTATCCGGAATTTGAA 780
751 ATTCATGTGGATGCGAGCAAGTGTGGATTTATGCAACCATTCCTTTATCCAGAGCTTGAA 810
781 TGGGACTTTAGATTCCTTGGTGAAGAGTATCAATGTGAGTGTGTCACAAATATGTTCTT 840
811 TGGGACTTTAGATTCCTTGGTGAAGAGTATCAATGTGAGTGTGTCACAAATATGTTCTT 870
841 GTGTACGCAAGGATTTGGTGGGTGATCTGCGAAGAACAAAGAGATTTGCCGTGAGAACTC 900
871 GTCTATGCTGGTATTTGGTGGGCCAATTTGGAGGAATAAGGAAGACTTTGCCCTGATGAAGCTT 930
901 ATCTTCCATCAATATCTTGGTGTCTGACCAACCCACTTTACTCTCAATTTCTCCAAA 960
931 ATTTTCCATCAATATCTTGGTGTCTGATCAACCTACTTTTCACTCTCAACTTCTCTAAA 990
961 GGTTCAGTCAAGTCAATGCTCAATATCTACCACTTATCCGATTTGGGCCACGAGGTTTAC 1020
991 GGTTCAGTCAAGTCAATGCTCAATATCTACCACTTATTCGCTTTGGGTTTGGAGGTTTAC 1050
1021 AGAATGATGATGAGAAATTTGAGAGAGATATGATGCTCTTAAAGGAGGACTTTGAGAG 1080
1051 AGAATGTTATGAGAAATTTGAGAGAAATTCAGAGGATTAAGAGAGGAAATTTGAGAA 1110
1081 ACAGAAAGTTCAACATGCTCTCAAAAGGACGAGGAGTGCCACTTTGCTGCTTTCTCTTG 1140
1111 AGTGAAGATTTCAACATAATCTCCAAAGAAATTTGGAGTTCCCTTTAGTAGCAATTTCTCTT 1170
1141 AAGATAGGAGCTGTCACTAGTTCGAAATCTCCGACATGCTTCGAGAGTATGGATGG 1200
1171 AAGAGAACAGTCAACCAATAGTTCGAAATTTCTGAAACTCTTTAGAGAAATTTGGAGTGG 1230
1201 ATAGTCCCGGCTTACCAATGCTCCAAATGCAACCAACATCACTGTTTCTTCTGTTGTT 1260
1231 ATGTTCTCTGATATCTATGCAACCAATGCTCAACATGTTTACAGTTCTCAGAGTTGTC 1290
1261 ATCAGAGAGAGATTTTCTCGAGAAACATCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320

576-820
e 820, Application US/09887576
No. US2002014407A1
INFORMATION:
ANT: Budworth, P.
ANT: Brown, D.
ANT: Chang, H.
ANT: Zhu, T.
ANT: Han, B.
ANT: Wang, X.
ANT: Cooper, Bret
OF INVENTION: Promoters for regulation of plant expression
REFERENCE: 1360.001US1
T APPLICATION NUMBER: US/09/887,576
T FILING DATE: 2001-06-25
APPLICATION NUMBER: US 60/213,848
FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/214,087
 PRIOR FILING DATE: 2000-06-23
 PRIOR APPLICATION NUMBER: US 60/258,692
 PRIOR FILING DATE: 2000-12-29
 NUMBER OF SEQ ID NOS: 875
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 820
 LENGTH: 1479
 TYPE: DNA
 ORGANISM: Oryza sativa
 -09-887-576-820

Query Match 55.3%; Score 834.2; DB 10; Length 1479;
 Best Local Similarity 75.9%; Pred. No. 2.3e-265;
 Matches 1031; Conservative 0; Mismatches 328; Indels 0; Gaps 0;

1 ATGGTGTCTCCACCGCGTATCGAGTCGAGTCCTCCGTCCTCACTCCACATTCGATCA 60
 1 ATGGTGTCTCCACCGCGTATCGAGTCGAGTCCTCCGTCCTCACTCCACATTCGATCA 60
 61 CTTTACGTCCTTCACTTCTTCAAGTTCAGATGCGGAAACTCGATTCTTCAAGGAA 120
 61 CGCTAGTCGCGCTCTCTCCAAAGTACCGGATGCGGAGAACTCGATCCGGAAGAG 120
 121 GCGGCTATCAGATCATCAACGACGAGTCGATGCTTGACGGGAATCCAGGTTGAATTA 180
 121 GCGGCTATCAGATCATCAACGACGAGTCGATGCTTGACGGGAATCCAGGTTGAATTA 180
 181 GCTCTCTTGTGACACATGATGAGGCTGAGTGTGATTAACATCATGCTCTCTCATC 240
 181 GGTCTGCTGTCACACGAGTGAAGGACCGAGTGGACAGTCAATCATGCGCCCATC 240
 241 AACAGAACTACGTCGACATGAGGAGTACCGGTCACCGGAGTCCAGAACCGGTGC 300
 301 GTGAACATGATGACATCTATTCATACCGGTTAGAGAGGCGGAGACCGCGTCCGA 360
 301 GTGAACATGATGACGACCTGTTCACGCGCGCTTCGGGAGGAGACGAGCGGTTGGC 360
 361 GTAGGAACCGTTTGGATCATCGAGGCGCATATGTTGGCGGTTTGGCTTCAAGCGTAA 420
 361 GTAGGACCGTGGTTCGTCGAGGCGCATCATGCTGGCGCGGCTTCAAGCGGCG 420
 421 TGGGACACAGCGCAAGCTGAAGGAAACCGGTCGATTAACCCAACTGTCCACGGA 480
 421 TGGGACACAGCGCAAGCGGAGGCGGAGCGGTTTCGACAGCGGCAACATCATCAGCG 480
 481 GCCAATGTTCAAGTGTGTTGGAGAAATTCGCTAGGTACTTGGAGTTGAATTAAGAA 540
 481 GCCAATGTTCAAGTGTGTTGGAGAAATTCGCTAGGTACTTGGAGTTGAATTAAGAA 540
 541 GTGAATTCAGTGAAGGATPACTATGATGGAACCTCAACAGCTGTTGATGTTGAT 600
 541 GTGAATTCAGTGAAGGATPACTATGATGGAACCTCAACAGCTGTTGATGTTGAT 600
 601 GAGACACCATTTGTTGCGGACATCTTGGTTCCTTCACTTAAATGAGATTCGAGAT 660
 601 GAGACACCATTTGTTGCGGACATCTTGGTTCCTTCACTTAAATGAGATTCGAGAT 660
 661 GTTAACTCTTGAACGATCTTGTGCGAAAGAAACGAGTGGGATGATACACCA 720
 661 GTTAACTCTTGAACGATCTTGTGCGAAAGAAACGAGTGGGATGATACACCA 720
 721 ATCCAGTGGATGCGGCAAGTGGAGATTCATGACCGGTTTTGATTCGGAATTTGAA 780
 721 ATCCAGTGGATGCGGCAAGTGGAGATTCATGACCGGTTTTGATTCGGAATTTGAA 780
 781 TGGGACTTTAGACTTCCCTTGGTGAAGATATCAATGTGAGTGTCAAGTATGACTT 840
 781 TGGGACTTTAGACTTCCCTTGGTGAAGATATCAATGTGAGTGTCAAGTATGACTT 840
 841 GTGTACCGAGGGATTGGTTGGGTGATCTCGGAAACAAAGAGGATTTGCTGAGAACTC 900

841 GTGTACCGCGCATCGGCTGGTGTGATCTGGGCAACAAGAGGAGACCTGCCGAGAGCTC 900
 901 ATCTTCCATATCAATATCTTGGTGTGATCTGACCAACCCAGCTTACTCTCAATTTCTCAA 960
 901 ATCTTCCATATCAATATCTTGGTGTGATCTGACCAACCCAGCTTACTCTCAATTTCTCAA 960
 961 GGTTCAAAGTCAAGTCTCAATATCTGATCAATATCTGATCAATATCTGATCAATATCTG 1020
 961 GGTTCAAAGTCAAGTCTCAATATCTGATCAATATCTGATCAATATCTGATCAATATCTG 1020
 1021 AGAATGTGATGAGGATTCGAGAGGATATGATGCTTAAAGGGAAGGACTTGAAG 1080
 1021 AGAATGTGATGAGGATTCGAGAGGATATGATGCTTAAAGGGAAGGACTTGAAG 1080
 1081 ACAGAAAGGTTCAACATGCTTCAAGGACGAGGAGTGCACATTTGCTGCTTTCTCCCTG 1140
 1081 ACAGAAAGGTTCAACATGCTTCAAGGACGAGGAGTGCACATTTGCTGCTTTCTCCCTG 1140
 1141 AAAGATAGCAGTGTCACTGATGTTGAAATCTCCGACATGCTTCGAGGATGATGATGG 1200
 1141 AAAGATAGCAGTGTCACTGATGTTGAAATCTCCGACATGCTTCGAGGATGATGATGG 1200
 1201 ATAGTCCCGGCTTACATGCTTCCAAATGCACACATCATCTGTTCTGCTGCTGTT 1260
 1201 ATAGTCCCGGCTTACATGCTTCCAAATGCACACATCATCTGTTCTGCTGCTGTT 1260
 1261 ATCAGAGAGATTTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
 1261 ATCAGAGAGATTTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
 1321 ATGCTGAGCTGATGAGTCTTCTTCGAGAGTGTATTCAC 1359
 1321 ATGCTGAGCTGATGAGTCTTCTTCGAGAGTGTATTCAC 1359

RESULT 10

US-10-167-547C-1
 ; Sequence 1, Application US/10167547C
 ; Publication No. US20030170653A1
 ; GENERAL INFORMATION:
 ; APPLICANT: E.I. du Pont de Nemours and Company
 ; APPLICANT: Damude, Howard G.
 ; TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
 ; FILE REFERENCE: Butyrolactone and its Intermediates
 ; CURRENT APPLICATION NUMBER: US/10/167,547C
 ; PRIOR FILING DATE: 2003-03-17
 ; PRIOR APPLICATION NUMBER: 60/297198
 ; PRIOR FILING DATE: 2001-06-08
 ; NUMBER OF SEQ ID NOS: 67
 ; SOFTWARE: Microsoft Office 07
 ; SEQ ID NO 1
 ; LENGTH: 1497
 ; TYPE: DNA
 ; ORGANISM: Alstroemeria
 US-10-167-547C-1

Query Match 51.4%; Score 775.4; DB 12; Length 1497;
 Best Local Similarity 70.6%; Pred. No. 7.5e-246;
 Matches 1066; Conservative 0; Mismatches 431; Indels 12; Gaps 2;

1 ATGGTGTCTCCACCGCGTATCGGAGTCGAGTCCTCCGTCCTCACTCCACATTCGATCA 60
 1 ATGGTGTCTCCACCGCGTATCGGAGTCGAGTCCTCCGTCCTCACTCCACATTCGATCA 60
 61 CGTTAGCTCCGTAATTCATCTTCTAGGTTCAAGATGCCGGAATACTCGATTCCTAAGGAA 120
 61 CGTTAGCTCCGTAATTCATCTTCTAGGTTCAAGATGCCGGAATACTCGATTCCTAAGGAA 120
 121 GCGGCTATCAGATCATCAACGACGAGTGTGATGCTTGAACGGAATCCACGTTGAATTA 180
 121 GCGGCTATCAGATCATCAACGACGAGTGTGATGCTTGAACGGAATCCACGTTGAATTA 180

181 GCCTCCCTTTGAGCAGCATGATGGAGCCTGAGTGTGATAAATACTCATATGTCCTCCATC 240
181 CGCTCGTTCTGTCACGACCTGATGGAGCCGAGTGGGATCGCTCATGATCGCCGCGCC 240
241 AACAAAGAACTATGTTGATGAGCAGTACCCCGTACCACACCGAACTTCAGAAACCGATGT 300
241 AACAAAGAACTATGTTGATGAGCAGTACCCCGTACCACACCGAACTTCAGAAACCGATGT 300
301 GTGAACATGATGTCACATCTATTCAATGACACCGTTAAGAGCGCGAGACCCGCGTGGAA 360
301 GTTAATAATATAGCCCACTCTTCAATGCGCCCTATTGGGATGAGGAAACAGCAGTAGGA 360
361 GTAGAACCCGTTTGATCATCGAGGCCATATGTTGCGCGGTTTGGCCCTCAAGCGTAAA 420
361 GTTGGGACAGTGGGGTCAATAGAAAGCAATATGCTTGAGGCTTGGCANTCAAGAGAAAG 420
421 TGGCAGAACCAAGCCAAAGCTGAAGGCCAAACCCGTCGATAAACCCCAATTTGTCCCGGA 480
421 TGGCAGAACCAAGCCAAAGCTGAAGGCCAAACCCGTCGATATGCAAGGCCCAATTTGTCCCGGT 480
481 GCCAATGTTCAAGTGTGTTGGGAGAAATTCGCTAGGTACTTTGAGGTTGAACTTAAGGAA 540
481 GCAACGTTTCAGGTTTCTGGGAGAAATTCGCTAGGTATTTTGAAGTTGAATCGAAGAA 540
541 GTGAAATGAGTGAAGGATCTATGTTGATGGACCCCTCAACAAAGCTGTTGATGTTGAT 600
541 GTGAAGCTGAGGAGGTTTATTACATCATGGACCCAGAGAAGGCTGTGAAATGTTGGAT 600
601 GAGAACCACTTGTGTTGGGACATCTTGGTTTCCACTTAAATGGAGAAATCGAAGAT 660
601 GAGAATACCAATGTTGTTGCTGATCTTGGGCTCAACCTTACTGAGAGAGTTTCAAGAT 660
661 GTTAAACTCTTGAACGATCTTCTTGGTGGAAAGAACAAAGAAACCCGATGGGATACACCA 720
661 GTTAAACTCTTGAACAACTCTTGAAGAGAGAAACAAAGAAACTGGTGGGACACACC 720
721 ATCCAGTGGATCGGCAAGTGGAGGATTCATTGCAACGTTTGTGATCGGAATGGA 780
721 ATTATGTTGATGCTGCTAGTGGTGGATTCATTGCTGCTTTCTATACCCAGAACTGGAA 780
781 TGGGACTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGGTCAAGATGAGACTT 840
781 TGGGATTTCCGATTTACACTGGTGAAGAGTATTAAATGTCAAGCGGACACAAATATGGCCTT 840
841 GTGTACCGAGGATTTGGTGGTCAATCTGAGAAACAAAGAGAGATTTGCTGAGGAATC 900
841 GTTTATGAGGTGGGTTGGGTTGTCTGAGGAAACAAAGAGATCTTCTGAAGAGCTC 900
901 ATCTTCCATATCAATATCTTGGTGGACCAACCCACCTTTTACTCTCAATTTCTCCAAA 960
901 ATTTTCCATATAAATACCTTGGGCGAGATCAGCTACTTTCCACCTCAATTTCTTAAA 960
961 GTTCAAGTCAAGTCAATGCTCAATCTCAATCTTCCGATTCGATTCGAGAGGTTAC 1020
961 GTTCAAGCCAGATAATGCTCAATATTTATCAATCTTCCGCTTGGTTTTCAGGGGAT 1020
1021 AGAATGTGATGAGAAATGTCAGAGAGATATGATCGTCTTAAGGGAAGGACTTGAAG 1080
1021 AAGACATAATGGAATCTGATGAGAAACAAAGAACTACTGAGAGAGGTTGAGAGG 1080
1081 ACAGAAAGGTTCAACATGCTTCAAGAGCAGGAGTGCCACTTGTGCGTTTCTCTTGG 1140
1081 ACGGCGCGTTTCGAGATAGTCTCAAAAGATATTGGGTTGCTCTTGTGATTTGCTCTC 1140
1141 AAAGATAGCAGTGTACACATGAGTTGGAATCTCCGACATGCTTCGAGGATGATGG 1200
1141 AAGACAGAGCCAGTACACTGTCTTTGAGATACCGGACCCCAATGAGAGGTTGAGATGG 1200
1201 ATGATGCGCGGCTACCAATCCCTCCAAATGCAACACATCTGTTCTTGTGTGGTT 1260
1201 ATCAATCTTGCAATACCAATGCCAAAGGACGAGGACATAGTGTCTCTCGGTGGTT 1260

Qy 1261 ATCAGAGAAGATTTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
Db 1261 ATCAGAGAAGATTTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
Qy 1321 ATCCGTGAGCTCGATGAGCTTCTTTCGAGAGTGTATCACAATAATACCTTTGGACAAGAG 1380
Db 1321 CTGGCTGAGCTGGAAGTACTTCC-----CAGTCGATCACCACCATTTGCCATGTT 1371
Qy 1381 AAGAGTAATCTAACAGCGATAACTTGTGTCACGTTGAGAGAGAGGATATCGACAAG 1440
Db 1372 ACGGCTG---TGAGAGAACGATAATGCGGAAGCTGTGATCAAGAAGAGTTTCTCTGGAGATA 1428
Qy 1441 CAGAGAGATATCATCACTGGCTGGGAAGATTTTGTGCCGACAGGAAGAACGAGTGGT 1500
Db 1429 GAGAAGAAGTTTATTACATTTGGAAGATGTAGTGTGAACGGCAGAGACTAATAAA 1488
Qy 1501 ATCTGCTAA 1509
Db 1489 GTTTGCTGA 1497

RESULT 11
US-10-167-547C-3
; Sequence 3, Application US/10167547C
; Publication No. US20030170653A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company
; APPLICANT: Damude, Howard G.
; TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
; FILE REFERENCE: Butyrolactone and its Intermediates
; FILE REFERENCE: C11804 US NA
; CURRENT APPLICATION NUMBER: US/10167,547C
; PRIOR FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/297198
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Microsoft Office 07
; SEQ ID NO 3
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Alstroemeria
US-10-167-547C-3

Query Match 49.8%; Score 751; DB 12; Length 1530;
Best Local Similarity 72.4%; Pred No. 9.6e-238;
Matches 973; Conservative 0; Mismatches 370; Indels 0; Gaps 0;

Qy 1 ATGGTGTCTCTCCACGCCGTATCGGAGTCGGAGCTCTCGTCCACTCCACATTCGATCA 60
Db 1 ATGGCTCTCTCCAGCGTCTCTCCGACTCCAAACAACCAAGTCGAGTCACCTATGCTCT 60
Qy 61 CGTTAGCTCGGTACTTCACTCTCTAGTTCAAGATGCCGGAACCTCGATTCTCTTAAGAA 120
Db 61 CGTTAGCTTCGAGCAGGCTCCAGGTTTCAAGATGCCGGAAGTCTGATACCAAGAG 120
Qy 121 GCGCGGTATCAGATCATCAACGACGAGTGTGATCTTGAACGGAATCCACGTTGAAC 180
Db 121 GCGCGGTACAGATGATCAACGACGAGTGTGATCTTGAACGGAACCCAGGCTGAAC 180
Qy 181 GCCTCTTTTGAAGCATGGAATGGAGCTGAGTGTGATTAACCTCATCTGCTCTCCATC 240
Db 181 GCTTCGTTGTCGACGACGTGATGGAGCGGAGTCCGATCGTCTGATGATGTCCACCATC 240
Qy 241 AACAGAATCTATGTTGACATGGACGAGTACCCCGTACCACCGAACTTTCAGAACCGATGT 300
Db 241 AACAGAATCTACGCCCTCATGACGATTTACCCGGTCACTATTGACATACAGATCGCTGC 300
Qy 301 GTGAACATGATTTGCAATCTATTCAATGCAACGCTTAGAAGAGCGGAGACCCGCTGGA 360
Db 301 GTGAATGATGATGCCAACCTCTTTAATGCGCAATTTGGGAGGGGGGAAACACAGTAGGA 360
Qy 361 GTAGGAACCGTTGAGATCATCGAGGCGCATTAATGTTGGCGGTTTGGCCCTTCAAGCGTAAA 420

361 TGTGCTACGCTGGGATCATCAGAACCCATGATGCTTGCAGGGTGGCATTCAGAGAAAT 420
421 TGGCAGAACAGCCAAAGCTGAAGGAAACCCGTCGATAAACCACCAATGTCCCGGA 480
421 TGGCAGAACAAAGAAAGGAGAGGGAAGCCATATGACAAAGCCCAACATGTCCACCGT 480
481 GCCAATGTTCAAGTGTCTTGGGAGAAATTCGCTAGGTACTTTGAGGTGCAACTTAAGAA 540
481 TCAAAATGTTAGGTTTGTCTGGGTGAATTCGCTAAGTATTTTGAAGTGAATGAAGAA 540
541 GTGAATTTAGGAGGAGATATTAATGTCATGGACCCAGAGAAGCTGTGAAATGGTGGAT 600
601 GAGAACACATTTGTGTTGGGACATTTCTTGGTTCACCTCTTAATCGAGAAATTCGAAGT 660
601 GAGATACCATTTGTGTTGGTGCATCTTGGGCTCGACCCCTTACTGGAGATTCGAAGT 660
661 GTTAAACTCTTGAACGATCTCTTGGTCGAAAGAAACAAAGAAACCCGATGGGATACCA 720
661 GTCAAACTGTAAAGACCTCTCTGTAGAGAGAACAGAAACTGTTGGGATACACC 720
721 ATCCACGTGATCGGCAAGTGGAGATTCATTGCAACCGTTTGTGATCGGAATTTGAA 780
721 ATTCAATGTTGATGCTGATTTGGTGGATTCATTGCTCCATTTATCTATCCAGAACTGGAA 780
781 TGGGACTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGGTCACAAAGTATGGACTT 840
781 TGGGATTTCCGACTACCTCTGTTGAGAGATCAATGTGAGTGAACACAAATACGSCCTT 840
841 GTGTACGAGGAGATTTGGTGGTGAATCTGGAGAAACAAAGAGATTTGCTGAGGAAGTC 900
841 GTCTATCCCGCGTGGTGGTGGTCTGTGAGGAAACAAAGAAATGATCTTCTGAAGAACTC 900
901 ATCTTCCATATCAATATCTTGGTGGTGAACAAACCCACCTTTTACTCTCAATTTCTCAA 960
901 ATTTTCCATATCAATATCTTGGGATTTGATCAACCCACTTTTACCTCACTTCTCGAA 960
961 GGTTCAAAGTCAAGTCAATGCTCAATACATCAACCTTATCCGATTTGGGCGACGAGGTTAC 1020
961 GGTTCAAACAGATAATTTGGTCAATATCTATCAATTAATTCGCTTGGTGGGCGTAC 1020
1021 AGAAATGTGATGGAGAAATTCAGAGAGAAATATGATCGTCTTAAGGGAAGGACTTGAAG 1080
1021 AAGATATAATGGAATACTGACGAGAAATTCAGAGAAATTTTAGGGAACATCTCGAGAG 1080
1081 ACAGAAAGGTTCAACATCGTCTCAAGAGCAGGAGTGCCATTTGTCGCTTTCTCCTTG 1140
1081 ATGGCGGTTTTCGAGATCATCTCAAGGATATTTGGGCGGCTCTCGTCACAATTTGCTCT 1140
1141 AAAGATAGAGTGTACACTGAGTTCGAATCTCCGACATGTTCCGAGGTATGGATGG 1200
1141 AAGACAGCAGAAACATAGTGTCTTTAAGATAGCCGATCAATTAGAGGTTTGGATGG 1200
1201 APATGCGCGGCTACAAATCCCTCCAAATGCAACACACATCATGTTCTTCTGTGGTT 1260
1201 ACAATTCCTGCATACAAATGCCAAGAGCCTTGGAGCAGATAGCCGCTCTCTGTGGTT 1260
1261 ATCAGAGAGATTTCTCGAGAACATCTGCTGAGAGACTTGTGATCGATAGAGAAAGTG 1320
1261 ATCAGGAGAGCTTCAGCGGAGGCTCCCGAGCGCTTACTGATGATGATGATGATGATG 1320
1321 ATGCGGTGAGCTCGATGAGCTTCC 1343
1321 TTGGTTGAGCTGGACATACATCC 1343

RESULT 12

US-10-167-547C-5
; Sequence 5, Application US/10167547C
; Publication No. US20030170653A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company

; APPLICANT: Demude, Howard G.
; TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
; FILE REFERENCE: Butyrolactone and its Intermediates
; CURRENT APPLICATION NUMBER: US/10/167,547C
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: 60/297198
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Microsoft Office 07
; SEQ ID NO 5
; LENGTH: 1590
; TYPE: DNA
; ORGANISM: Alstroemeria
US-10-167-547C-5

Query Match 49.8%; Score 751; DB 12; Length 1590;

Best Local Similarity 72.4%; Pred. No. 9.8e-238;

Matches 973; Conservative 0; Mismatches 370; Indels 0; Gaps 0;

Qy	1	ATGGTGCTCTCCCAAGCGCTATCGGAGTCGGAGCTGCTCGTCCACTCCACATTCGCATCA	60
Db	1	ATGGCTCTCTCCAGCGTCTCTCCGACTCCAAACCAAGTGCAGTGCACCTATGCTCT	60
Qy	61	CGTTACGTCCGTACTTCACTTCTCTAGTTCAAGATGCGCGGAAAACTCGATTCTTAAGGAA	120
Db	61	CGTTACGTTCGCGACGAGGCTCCAGGTTTCAGGATGCGCGAGAGTCGATACCAAGAG	120
Qy	121	GCGCGGTATCAGATCATCAACGACGAGCTGCTTGAAGGGAATCCACGGTTGAACCTTA	180
Db	121	GCGCGGTTACGATGATCAACGACGAGCTGCTGCGAGGAGACCCAGGCTGACTTG	180
Qy	181	GCCTCTCTTGTGACGATGGATGGAGCTGAGTGAATAACTCATCATGTCCTCCATC	240
Db	181	GCCTCTCTGTCGACGAGTGGATGGAGCCGAGTGCATGCTCATGATGTCACCATC	240
Qy	241	AACAGAGACTATGTTGACATGGAGTACCCCGTACACCGAGCTTCAGAACCGATGT	300
Db	241	AACAGAGACTATCCGCTCATGGACGATTTACCGGTCATTTGACATACAGATCGCTGC	300
Qy	301	GTGAACATGATTGCACATCTATTCAAATGACCCGTTAGAGAGCGGAGACCCGCTCGGA	360
Db	301	GTGAATATGATAGCAACCTCTTTAATGCGCAATTTGGGAGGGGGAACACACAGTAGGA	360
Qy	361	GTAGGACCGTTCGATCATCGGAGGCTAATGTTGGCGGTTTGGCCCTTCAAGCGTAA	420
Db	361	TGTCCTACGTTGGATCATCAGAGCCATGATGTTGAGGTTTGGCATTCAGAGAAAT	420
Qy	421	TGGCAGAACAAAGCGCAAGCTGAAGCAACCCGTCGATAAACCACATTTGTCAACCGGA	480
Db	421	TGGCAGAACAAAGAGAGGAGAGGGGAGGAGCCATATGACAGGCCCAACATGTCACCGGT	480
Qy	481	GCCATGTTTCAAGTGTGTTGGGAGAAATTCGCTAGTACTTTGAGGTTGMACTTAAGGA	540
Db	481	TCAAAATGTTTCAAGGTTTGTGGGTGAAATTCGCTAAGTATTTTGAAGTTGAAATGAAAA	540
Qy	541	GTGAAATGAGTGAAGGATATGATGATGGAGCCCAAGAGCTGTTGATATGTTGAT	600
Db	541	GTGAAATTTGAGGAGGAGATATGATGATGGAGCCCAAGAGAGCTGTGGAATGTTGAT	600
Qy	601	GAGAACCAATTTGTTGGGAGCATTTGTTGCTCACTCTTAATGGAGAAATTCGAAGAT	660
Db	601	GAGAAATACCAATTTGTTGCTGCCATCTTTGGGCTCGACCTTACTGAGAGGTTTCAAGAT	660
Qy	661	GTTAAACTCTTGAACGATCTCTTGGTCGAAAGAAACAAAGAAACCCGATGGGATACCA	720
Db	661	GTCAAACTGTAAACGACCTCTCTGTAGAGAGAACAGAAACTGTTGGGATACACC	720
Qy	721	ATCCACGTGATCGGCAAGTGGAGATTCATTGCAACCGTTTGTATCCGGAATTTGAA	780
Db	721	ATTCATGTTGATGCTGCTATTGTTGGATTCATTGCTCCATTTATCTATCCAGAACTGGA	780
Qy	781	TGGGACTTTAGACTTCCCTTGGTGAAGAGATATCAATGTGAGTGGTCCACAGTATGACTT	840

781 TGGGATTTCCGACTACCTCTCTGGTGAAGATATCAATGTCTAGTGGACACAAATACCGCCTT 940
841 GTGTACGCGGATTTGGTGGGTGATCTGGAGAAACAAAGAGGATTTGCCGTGAGAACTC 900
841 GTCTATCCGGCGTGGTGGGTGCTCTGGAGGAAACAAAGATGATCTTCTGTAAGAACTC 900
901 ATCTTCCATATCAATATCTGGTGGTCTGGACCAACCGACCTTTACTCTCAATTTCTCCAA 960
901 ATTTTCCATATCAATATCTGGGATTTGATCAACCCCACTTTTACCCCTCAACTTCTCGAA 960
961 GGTTCAGAGTCAAGTCAATGTCTCAATCTTACCACTTATCCGATTTGGGCCACGAGGGTTAC 1020
961 GGTTCAGAACAGATAATTTGGTCAATCTATCAATTAATTCGCTTGGTTTGGAGGGTAC 1020
1021 AGAATGTGTAGTGAATTTGAGAGATGATCGTCTTACGGGAGACTTGGAG 1080
1021 AAGAATATAATGGAATCTGACGAGAGATGCAAGAAATCTTAGGGAACATCTCGAGGAG 1080
1081 ACAGAAAGGTTCAACATCGTCTCAAGGACGAGGGAGTGCCACTTGTTCGCTTTCTCCTTG 1140
1081 ATGGCGGTTTCGAGATCATCTCCAAGGATATTGGGGCGCTCTCGTCACAATTTGCTCTC 1140
1141 AAGATAGAGCTGTCACTAGTTCGAATCTCCGACATGCTTCGACGATGATGG 1200
1141 AAGGACAGCAAAACATAGTGTCTTTAAGATAGCCGATACAAATTAGAAGGTTTGGATGG 1200
1201 ATAGTGGCGGCTTACACATGCTCTCAAGGACGAGGGAGTGCCACTTGTTCGCTTGGTT 1260
1201 ACAATTCCTGCATACAAATGCCAAGGACGTTGAGCACATAGCCGCTCTCTGTGGTT 1260
1261 ATCAGAGAAAGATTTCTGAGAACACTCTCGTGAAGACTTGTGATCGATATAGAGAAAGTG 1320
1261 ATCAGGAGGACTTTCAGCGGAGCGCTCGCGAGCGCTCGCGAGCGCTAGTATGACATGAAGAGG 1320
1321 ATGCGTGAGCTCGATGAGCTTCC 1343
1321 TTGGTTGAGCTGGACATACATCC 1343

RESULT 13

S-10-006-852-17

Sequence 17, Application US/10006852

Publication No. US20030046732A1

GENERAL INFORMATION:

APPLICANT: Kinnersely, Alan M.

APPLICANT: Furano, Frank J.

TITLE OF INVENTION: Methods for Regulating Plant GABA Production

FILE REFERENCE: 7224-65

CURRENT APPLICATION NUMBER: US/10/006,852

CURRENT FILING DATE: 2002-07-01

PRIOR FILING DATE: 2002-07-01

PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patent in version 3.1

SEQ ID NO 17

LENGTH: 1783

TYPE: DNA

ORGANISM: Lycopersicon esculentum

FEATURE:

NAME/KEY: CDS

LOCATION: (6)..(1511)

OTHER INFORMATION:

US-10-006-852-17

Query Match 48.8%; Score 736.6; DB 14; Length 1783;
Best Local Similarity 71.8%; Pred. No. 6.4e-233;
Matches 984; Conservative 0; Mismatches 379; Indels 0; Gaps 0;

Query 20 TATCGAGTCGAGAGCTTCCGCTCCACTCCACATTCGACATCGATCGTACGCTACTTAC 79

Db 28 TAAGAGATTGAGAGAGCTTGCCTGTACATTTGCATCAAGATATGTACAGGAAGCTT 87

Qy 80 TTCTAGTTCAGATGCGCGGAAACTCGATTTCTTAGGAAAGCGGCTATCAGATCATCA 139
Db 88 TACCTAAGTTTCAAAATGCTTAAAAAATCCATGCCGAAAGAGAGCTTATCAGATTGTA 147
Qy 140 ACGACGAGCTGATGCTTGACGGGAATCCACGGTTGAACCTTAGCTCCTCTTGTGAGCAT 199
Db 148 ACGACGAGCTTATGTTGGATGTAACCCAGGTTGAATTTAGCTTCTTGTAGCAT 207
Qy 200 GGATGAGAGCTGAGTGTGATAAATCATCATGATCTCTCCATCAACAGAACTATGTTGACA 259
Db 208 GGATGAGAGCTGAGTGTGATAAATCATCATGATCTCTCCATCAATATAAATACTATGTCGACA 267
Qy 260 TGGACGAGTACCCCGCTCACCCAGAACTTCAGAACCGATGTGTGAACATGATTCACATC 319
Db 268 TGGATGAGTATCTGTGACCACTGAACCTTCAAAATAGATGTGTAAACATGTTAGCATC 327
Qy 320 TATTCAATGACAGCTTAGAAGAGCGGAGACCGCGCTCGAGTAGGAGACCGTTGGATCAT 379
Db 328 TTTTCCATGCCCCGGTTGGTGTGATGATGAGACTGSCAGTTGGTACAGTGGGTTTCA 387
Qy 380 CGGAGGCCATAATGTTGGCGGTTTGGCCCTTCAAGCCTAAATGGGAGAAACAAGCGCAAAG 439
Db 388 CAGAGCAATAATGCTTGTCTGGCCCTTCTTCAAACGCAATGGCAATCGAAAAGAAAG 447
Qy 440 CTGAGGCAAAACCGCTGATATAAACCACATTTGTCTACCGGAGCCAAATGTTCAAGTGTGT 499
Db 448 CAGAAGCAAAACCTTTCGATAAGCTTAATATAGTCACTGGAGCTAATGTGACAGTCTGT 507
Qy 500 GGGAGAAATTCGCTTAGTACTTTGAGGTTGAACTTAAGGAAGTGAATGAGTGAAGGAT 559
Db 508 GGGAAATTTGAAAGTATTTTGAAGTTGAGTTGAGAGGTTGAACTTAAGAAAGAGAT 567
Qy 560 ACTATGATGAGTGGACCTTCAACAGCTTTGATATGTTGATGAGAACACCACTTTGTTG 619
Db 568 ACTATGATGAGTGGACCTTCAACAGCTTTGATATGTTGATGAGAACACCACTTTGTTG 627
Qy 620 CGGACATTTCTGTTTCCACTTAAATGGAGAAATTCGAAGATGTTAAACTCTTGAACGATC 679
Db 628 CTGCAATCTTGGTTTCTACTCTGCTGGGAGTTTGAAGATGTTGAAGCTCTTAAACGAGC 687
Qy 680 TCTTGTGCAAGAAACAAAGAACCGGATGGGATACACCAATCCACGTTGGATGGGCAA 739
Db 688 TCTTTCACAAAAGAAACAAAGAAACCGGATGGGAGACACCGATTCATGTCGATGCTGCGA 747
Qy 740 GTGAGGATTCATTTGACCGGTTTGTATCCGAAATTTGAATGGGACTTTAGACTTCCCT 799
Db 748 GTGAGGATTTATTTGCTCTTCTCTGCGGAGCTTGAATGGGATTTCCGTTTGCCTC 807
Qy 800 TGGTCAAGAGTATCAATGTGAGTGGTCAACAGTATGGACTTTGTGACGAGGAGTTGGTT 859
Db 808 TTGTGAAAAGTATAAATGTCAGCGGTACAAAGTATGGCTTTGTATATGCTGCTGCTGGTT 867
Qy 860 GGGTATCTGGAGAAACAAAGAGATTTGCCTGAGAACTCATCTTCCATATCAATATC 919
Db 868 GGGTATATGCGGAGCAAGAGAGCTTGCCTGAGAACTCATCTTCCATATCAATATC 927
Qy 920 TTGGTGTGACCAACCCACCTTTACTCTCAATTTCTCAAAAGTTTCAAGTCAAGTCAATG 979
Db 928 TTGGTGTGATCAGCCTTACTTTTACTCTCACTTCTCTAAAGTTTCTTATCAATAATG 987
Qy 980 CTCATATCTACCAACTTATCCGATTTGGCCACAGAGGTTACAGAAATGTGATGGAGAT 1039
Db 988 CACAGTATTATCAGTTAATAAGACTTTGGCTTTTGAAGGTTTATGAAGACGTCATGAAGAAT 1047
Qy 1040 GCAGAGAGATATGATCGTCTTAAGGAAAGGACTTGAAGAGACAGAAAGTTCAACATCG 1099
Db 1048 CTTTATCAACAGCAAAAGTACTTAACAGAGGAAATCAGAAAATGGGCGGTTTCGATATG 1107
Qy 1100 TCTCAAGAGCAGGGAGTCCACTTGTGCTTTCTTGAAGATAGCAGCTGTCTACA 1159
Db 1108 TCTCTAAGGATGTGGTGTCTCTGTTAGTACTTTTCTCTCAGGAGACAGCAAAATATA 1167
Qy 1160 CTGAGTTCCGAATCTCCGACATGCTTCGAGGATGATGATGATGATGCGGCTACACAA 1219

[illegible]

SULT 14
-03-727-758-1
Sequence 1, Application US/09727758
Publication No. US20030101487A1
GENERAL INFORMATION:
APPLICANT: KISAKA, HIROAKI
APPLICANT: KIDA, TAKAO
TITLE OF INVENTION: A method for producing transgenic plants having improved amino acid
TITLE OF INVENTION: composition
FILE REFERENCE: 200397US0
CURRENT APPLICATION NUMBER: US/09/727,758
CURRENT FILING DATE: 2000-12-04
PRIOR APPLICATION NUMBER: JP 11-352552
PRIOR FILING DATE: 1999-12-13
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1

Query Match 47.1%; Score 711.4; DB 11; Length 1180;
Best Local Similarity 75.7%; Pred. No. 1.1e-224;
Matches 894; Conservative 0; Mismatches 286; Indels 1; Gaps 1;

112	CCTAAGGAAGCGGGTATCAGATCATCAACGACGAGCTGATCCTTGACGGGAATCCACGG	171	1	CCAAAGGAAGCAGCATATCAGATTCATAATGATGAACTTATCTAGATGGAAATCCCAAGG	60
172	TTGAACCTTAGCCTCCTTTGTGACGATGATGGAGCCGTGAGTGTGATAAATACTCATCATG	231	61	TTGAATTTGGCATCTTTTGTGACAAATGATGGAAACCAAGATGTGACAAATTTGATGATG	120
232	TCCTCCATCAACAGAAGAACTATGTTGACATGCGAGGTACCCGGTCACCACCGAACTTCAG	291	121	GATTCCTAATAACAAAAATATGTTGACATGGATGAATAATCCTGTCAACACTGAGCTTCAG	180
292	AACGATGTGTGAACATGATTGCACATCTATTCANTGCACCGTTAGAGAGGCGGAGACC	351	181	AATCGGTGTGTAAACATGATAGCGCATTTATTTAATGCAACCACTTGAAGATGGAGAAACT	240
352	GCCGTCGAGTAGGAACCGTTGGATCATCGAGGCGCAATAATGTGGCCGGTTTGCCCTTC	411	241	GCAGTTGGAGTTGGAACAGTTGGTTCTTCAGAAGCCATTTATGCTTGTGATGGCCCTTT	300
412	AAGCGTAAATGGCAGAACAGCGCAAGAGCTGAAGGCAAAACCGTCGTATTAACCCCAACTT	471	301	AAGAGAAATGGCAAAACAAATGAAGCCCAAGGAAAGCCCTTATGATAAGCCCAACATT	360
472	GTACCGGAGGCAATGTTCAAGTGTGTGGGAGAAATTCGCTAGGTACTTTTCAGGTTGAA	531	361	GTACTGGTCTATGTCCAGGTGTGTGGGAAAAATTTGCAAGGTATTTTGAAGTTGAG	420
532	CTTAAGGAAGTGAATTAAGTGAAGGATACTATGTGATGGAACCTTCAACAGACTGTTGAT	591	421	CTTAAAGAAAGTGAAGTTGACTGATGGTACTATGTGATGAGCCCTGAGAAGCTGTGAA	480

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 782
LENGTH: 1455
TYPE: DNA
ORGANISM: Oryza sativa
-09-887-576-782

Query Match 47.0%; Score 709.6; DB 10; Length 1455;
Best Local Similarity 71.8%; Pred. No. 5.1e-224;
Matches 928; Conservative 0; Mismatches 364; Indels 0; Gaps 0;
/ 45 CTCACATTCCGATACAGTTACGTCGCTACTTCACTTCTAGGTTCAAGATCCCGGAAA 104
> 42 CTCACGTTTCGCTCGGGTACGTGCGCAGCGGCTCCGAGGTTTCAGATGCGGAGAA 101
/ 105 CTCGATTCTTAAGAGAGCGGCTATCAGATCATCAACGACGAGCTGATGCTTGACGGGAA 164
o 102 GTCGATCCCAAGGACCGCGCGTACCAGATCATCAACGACGAGCTGATGCTCGACGGCAA 161
/ 165 TCCACGGTTGAACTTAGCCCTCTTGTGACGACATGGATGGAGCTGAGTGTGATAACT 224
b 162 CCCGGCTGAACTTGGCGTCTTCTGTACACGCTGATGGAGCCCGAGTGGACAGCT 221
/ 225 CATCATGCTCTCATCATAAAGAACTATGTTGACATGGAGAGTACCCCGTCAACACGA 284
b 222 CATGATGGCGCCCATCAACAGAACTACGTCGACATGGATGAGTACCCCGTCAACCCGA 281
/ 285 ACTTCAGAACCGATGTGTGAACATGATTCACATCTATTCAATGACCGTTAGAGAGGC 344
b 282 GCTCCAGAACCGGTGCTGAACATGATCGGCTCTGTTCAACGCGCGATCGGGACGA 341
/ 345 GGAGACCGCGTCGAGTAGGAACCGTTGATCATCGGAGGCCATAATGTTGGCGGTTT 404
b 342 CGAGACCGCGCTCGGGTGGGCAACGTCGCGGCTGTCGAGGCGCATCATGCTGGCGGGCT 401
/ 405 GGCCTTCAAGCGTAAATGGCAGAACAAAGCGAAAGCTGAAGCAACCCGTCGATAAAC 464
b 402 GGCCTTCAAGAGGAGTGGCAGACAGGATGAAGCCGAGGGAGCCCGACGACAGCC 461
/ 465 CAACATTTGACCGGAGCAGTGTTCAGTGTGTTGGGAGAAATTCGCTAGGTACTTTGA 524
b 462 CAACATCGTACCGGGGCCAACGTCGAGTGTGCTGGGAGAAAGTTGCGCGCTACTTCGA 521
/ 525 GGTGAACTTAAAGGAGTGAATTTGAGTGAAGGATATGATGATGGACCCCTCAACAGC 584
b 522 GGTGAGCTCAAGGAGTGAAGTGAACCCAGGTTACTACGTGATGAACCCGAGAGGC 581
/ 585 TGTGATATGTTGATGAGAACCAATTTGTTGTCGACATCTTGTTCACCTTTAA 644
b 582 CGTGGAGATGGTCAGAGAACCAATCTGCGTCGCGCCATCTCGGGTCCACCTCAA 641
/ 645 TGGAGAAATTCGAGATCTTAACTCTTGAACGATCTCTTGGTCGAAAGAACAAAGAAC 704
b 642 CGCGAGTTCGAGGAGTCAAGATGCTCAACGACTCTCTCACCGCCAGAGCGCGAGAC 701
/ 705 CGGATGGATACACCAATCCAGCTGAGTGGGAGGAGGAGGATTCATGACCGTTT 764
b 702 AGGTGGAACACGCGCATCCATGGAACGCGGAGCGCGGTTTCATGCGCGCTTCAT 761
/ 765 GTATCCGGAATTTGAATGGACTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGG 824
b 762 CTACCGGAGCTGGAGTGGGACTTCCGGCTGCGCTGCTGTTGAGAGCATCAAGCTCAGCGG 821
/ 825 TCACAGTATGGACTTGTGACGAGGAGTGGTTGGGTGATCTGGAGAAACAAAGAGGA 884
b 822 CCACAGGTACCGGGCTCTCTACGCGGCGTGGGTGGGTCACTGGCGCAACAGGAGGA 881
/ 885 TTGCTTGAGGAATCATCTTCCATATCAATATCTTGGTGTGACCAACCCACCTTTAC 944
b 882 CTTCCCGGATGAGCTCATCTTCCACATCACTACTCTGGCGCGACCCAGCCACTTCAC 941
/ 945 TCTCAATTTCTCCAAAGGTTCAAGTCAAGTCAATGTTCAATACTACCAACTTATCCGATT 1004
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Db 942 GCTCAACTTCTCCAAAGGATCGAACAGATAATTGGCGAGTATTACCACCTCATTCGTCT 1001
QY 1005 GGGCCACGAGGTTTACAGAAATGTGATGGAGAAATTCAGAGAGAAATATGATCGTCTTAAG 1064
Db 1002 CGGATTCGAGGGGTACAAGGACATCATGAGAACTGCCGGGACACACGCGGTGCTCG 1061
QY 1065 GGAAGGACTTGAGAAGACAGAAAGGTTCAACATCGTCTCAAAGGACGAGGAGTGCCT 1124
Db 1062 GGAGGGATCGAGAAGACGGGCCACTTCGACGTGGTGTCAAGGACTCCGGCGTGCCGT 1121
QY 1125 TGTGCTTTCTCTTTGAAAGATAGCAGCTGTCACTGAGTTGAAATCTCCGACATGCT 1184
Db 1122 GGTGGCCTTCTCCCTCAAGGACTCGTCGCGGTACACGGTGTTCGAGGTGGCCGAGAGCT 1181
QY 1185 TCGCAGGTATGATGGATAGTGGCGCTACAAATGCCCTCCAAATGCACACATCAC 1244
Db 1182 CGCGCGCTTCGCGCTGGATCGTCGCGGCTACACCTGCCCGCGAGCTGAGACGTCG 1241
QY 1245 TGTCTTCTGTTGTTATCAGAGAGATTTCTCGAGAACACTCGCTGAGAGACTTGTGAT 1304
Db 1242 CGTGATGCGCTCGTTCATCCGAGGACTTCAGCCGGGCTCGCGAGGCTCATCAC 1301
QY 1305 CGATATAGAGAAAGTGTGCTGAGCTCGATG 1336
Db 1302 CGACCTCACAGACGCTGGCCGATATGGACG 1333

Search completed: October 22, 2003, 15:04:15
Job time : 439 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 nucleic - nucleic search, using sw model
 n on: October 22, 2003, 10:35:12 ; Search time 117 Seconds
 (without alignments)
 5692.711 Million cell updates/sec
 title: US-10-006-852-1
 rfect score: 1509
 quence: 1 atgtgtctctccacgcgt.....agacgagtgtatctgtaa 1509
 oring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0
 arched: 569978 seqs, 220691566 residues
 tal number of hits satisfying chosen parameters: 1139956
 inimum DB seq length: 0
 aximum DB seq length: 2000000000
 ost-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries
 atabase : Issued Patents NA:
 1: /cgn2_6/prodata/2/ina/5A COMB.seq:
 2: /cgn2_6/prodata/2/ina/5B COMB.seq:
 3: /cgn2_6/prodata/2/ina/6A COMB.seq:
 4: /cgn2_6/prodata/2/ina/6B COMB.seq:
 5: /cgn2_6/prodata/2/ina/PCtUS COMB.seq:
 6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736.6	48.8	1793	2	US-08-522-421-8
2	311.2	20.6	4403265	3	US-09-103-840A-2
3	311.2	20.6	4411529	3	US-09-103-840A-1
4	270.6	17.9	5565	3	US-09-068-193-21
5	133	8.8	36941	4	US-08-311-731A-130
6	64	4.2	359	4	US-09-056-556-192
7	64	4.2	359	4	US-09-072-596-187
8	41.6	2.8	7218	1	US-08-232-463-14
9	39.2	2.6	1230025	4	US-09-198-452A-1
10	25.8	2.4	16442	3	US-08-781-891-208
11	35.8	2.4	16442	4	US-09-618-166-208
12	35.6	2.4	15016	4	US-09-601-198-60
13	33.6	2.2	515	4	US-09-026-408-11
14	33.4	2.2	2004	1	US-08-471-033-18
15	33.4	2.2	2004	2	US-08-471-044-18
16	33.4	2.2	2004	2	US-08-463-483A-18
17	33.4	2.2	2004	2	US-08-471-046A-18
18	33.4	2.2	2004	2	US-08-470-566B-18
19	33.4	2.2	2004	2	US-08-469-334-18
20	33.4	2.2	2004	3	US-09-300-529-18
21	33.4	2.2	2576	1	US-08-471-033-35
22	33.4	2.2	2576	2	US-08-471-044-35
23	33.4	2.2	2576	2	US-08-463-483A-35
24	33.4	2.2	2576	2	US-08-471-046A-35
25	33.4	2.2	2576	2	US-08-470-566B-35
26	33.4	2.2	2576	2	US-08-469-334-35
27	33.4	2.2	2576	3	US-09-300-529-35

ALIGNMENTS

RESULT 1
 US-08-522-421-8
 ; Sequence 8, Application US/08522421
 ; Patent No. 5908973
 ; GENERAL INFORMATION:
 ; APPLICANT: Abu-Bakar, Umi Kalsom
 ; APPLICANT: Barton, Sarah Louise
 ; APPLICANT: Gallego-Veigas, Pedro Pablo
 ; APPLICANT: Gray, Julie Elizabeth
 ; APPLICANT: Grierson, Donald
 ; APPLICANT: Lowe, Alexandra Louise
 ; APPLICANT: Picton, Steve
 ; APPLICANT: Whorton, Lee Colin
 ; TITLE OF INVENTION: DNA, DNA CONSTRUCTS, CELLS AND PLANTS
 ; TITLE OF INVENTION: DERIVED THEREFROM
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, L.L.P.
 ; STREET: 1100 New York Avenue, N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20005-3918
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Microsoft Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/522,421
 ; FILING DATE: 11-JAN-1996
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9305868.3
 ; FILING DATE: 22-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9305869.1
 ; FILING DATE: 22-MAR-1993
 ; APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9305859.2
 ; FILING DATE: 22-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9305865.9
 ; FILING DATE: 22-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9305866.7
 ; FILING DATE: 22-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9305867.5
 ; FILING DATE: 22-MAR-1993

28 33.4 2.2 2655 1 US-08-471-033-17 Sequence 17, Appl
 29 33.4 2.2 2655 1 US-08-471-033-26 Sequence 26, Appl
 30 33.4 2.2 2655 2 US-08-471-044-17 Sequence 17, Appl
 31 33.4 2.2 2655 2 US-08-471-044-26 Sequence 26, Appl
 32 33.4 2.2 2655 2 US-08-463-483A-17 Sequence 17, Appl
 33 33.4 2.2 2655 2 US-08-463-483A-26 Sequence 26, Appl
 34 33.4 2.2 2655 2 US-08-471-046A-17 Sequence 17, Appl
 35 33.4 2.2 2655 2 US-08-471-046A-26 Sequence 26, Appl
 36 33.4 2.2 2655 2 US-08-470-566B-17 Sequence 17, Appl
 37 33.4 2.2 2655 2 US-08-470-566B-26 Sequence 26, Appl
 38 33.4 2.2 2655 2 US-08-469-334-17 Sequence 17, Appl
 39 33.4 2.2 2655 2 US-08-469-334-26 Sequence 26, Appl
 40 33.4 2.2 2655 3 US-09-300-529-17 Sequence 17, Appl
 41 33.4 2.2 2655 3 US-09-300-529-26 Sequence 26, Appl
 42 33.4 2.2 4031 1 US-08-471-033-49 Sequence 49, Appl
 43 33.4 2.2 4031 2 US-08-471-044-49 Sequence 49, Appl
 44 33.4 2.2 4031 2 US-08-463-483A-49 Sequence 49, Appl
 45 33.4 2.2 4031 2 US-08-471-046A-49 Sequence 49, Appl

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305860.0
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305862.6
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9314351.9
 FILING DATE: 12-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9320988.0
 FILING DATE: 12-OCT-1993
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: ERTD1
 US-08-522-421-8

Query Match 48.8%; Score 735.6; DB 2; Length 1783;
 Best local Similarity 71.8%; Pred. No. 4.2e-232;
 Matches 964; Conservative 0; Mismatches 379; Indels 0; Gaps 0;

20 TATCGGAGTCGGAGCTCTCCGTCACCTCCACATTCGCACTGACGTTACGTCGCTAGCTTCAC 79
 28 TAAGAGATTGAGAGAGAGCTTGCACCTGATGATTTGCACTCAAGATATGTACAGGAACCTT 87
 80 TTCTAGGTTCAAGATGCGGAAATCTCGATTCCTTAAGAGAGCGGCTATCGATCATCA 139
 88 TACCTAAGTTCAAAATGCCCTAAATAATCCATCCGAAAGAGCAGCTTATCAGATTGTA 147
 140 ACCAGAGCTGATGCTTGAAGGAAATCCAGGTTGAATCTAGCTCTCTTGTGAGACAT 199
 148 ACAGAGGCTATGTTGGATGTTAAGGAGGTTGATTTAGCTTCTCTTGTAGCAGAT 207
 200 GGATGAGCTGATGATGATTAATCTCATGATGCTCCATCAAGAGAACTATGTTGACA 259
 208 GGATGAGGCGGAGTGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 267
 260 TGAAGAGTACCTGCTGACAGGAGTGCATGATGATGATGATGATGATGATGATGATGATG 319
 268 TGAAGAGTACCTGCTGACAGGAGTGCATGATGATGATGATGATGATGATGATGATGATG 327
 320 TATTCAATGACCGTTAGAGAGCGGAGACCGCGCTCGAGTATGAGAACCGTTGGATCAT 379
 328 TTTTCCATGCCCCGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATG 387
 380 CGGAGGCTAATGTTGGCGGTTTGGCGTTTGGCGTTTGGCGTTTGGCGTTTGGCGTTTGG 439
 388 CAGAGGCAATTAATGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 447
 440 CTGAAGCAAAACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 499
 448 CAGAGGCAAAACCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 507
 500 GGGAGAAATTCGCTAGTATCTTTGAGGTTGAATCTTAAGGAGTGAATTTGAGTGAAGAT 559
 508 GGGAGAAATTCGCTAGTATCTTTGAGGTTGAATCTTAAGGAGTGAATTTGAGTGAAGAT 567
 560 ACTATGATGAGGAGGCTTCAAGAGGTTTGAATGATGATGATGATGATGATGATGATGATG 619
 568 ACTATGATGAGGAGGCTTCAAGAGGTTTGAATGATGATGATGATGATGATGATGATGATG 627
 620 CGGACATCTTGTGTTCCATCTTTAATGAGAAATTCGAAGATGTTAACTCTTTGAACGATC 679
 628 CTGCAATCTTGTGTTCCATCTTTAATGAGAAATTCGAAGATGTTAACTCTTTGAACGATC 687
 680 TCTTGTGCAAGAGCAAAAGAGAGGAGTGGATGATGATGATGATGATGATGATGATGATG 739

688 TCCTTACAAAAAGAAACAAGGAAACCGGATGGAGACACCGGATTCATGTCGATGCTGCGA 747
 740 GTGAGGATTCATTCACCGTTTTCGATTCGGAATTCGGAATTCGGAATTCGGAATTCGCT 799
 748 GTGAGGATTCATTCACCGTTTTCGATTCGGAATTCGGAATTCGGAATTCGCTGCTC 807
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 808 TTTGAAAAAGTATAAATGTGAGGCTCAAGTATGGCTTGTATATGCTGCTGCTGCTGCT 867
 860 GGTGATCTGGAGAAACAAGAGGATTTGCTGCTGAGGAACTCATCTCCATATCAATATC 919
 868 GGTGATATGGCGAGCAAGAGGACTTTGCCGATGAACTGCTCTTTCATATAAATAC 927
 920 TTTGCTGCTGACCAACCCACCTTTACTCTCAATTTCTCCAAAGGTTCAAGTCAAGTCATTG 979
 928 TTTGGGTCGATCAGGCTACTTTTACTCTCAATTTCTCTTAAAGGTTCTCTATCAATATTG 987
 980 CTCATATCTACCACTTATCCGATTTGGGCCAGGAGGTTACAGAAATGTGATGGAGATT 1039
 988 CACAGTATTCAGTTTAAAGACTTGGCTTTGAGGTTTAAAGAACTCATGAGGAATT 1047
 1040 GCAGAGAGAAATATGATCGTCTTAAGGAGGACTTTGAGAGACAGAAAGTTCAACATCG 1099
 1048 GCTTATCAACCGAAAGTACTTAAAGAGGATCAAGAGGATCAAGAAATGGGCGGTTTCGATATTG 1107
 1100 TCTCAAAGAGAGGAGTGGCCTTGTGCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1159
 1108 TCTCAAAGAGTGGGTTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1167
 1160 CTGAGTTCCGAATCTCCGACATGCTTCCGAGGTATGGATGGATGGATGGATGGATGGAT 1219
 1168 CGTATTTGAGTATCTGAGATCTCAAGAGATTTGATGATGATGATGATGATGATGATGAT 1227
 1220 TGCTCCAAAGCACAACATCATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1279
 1228 TGCCACCGGATGCTGAACACATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1287
 1280 GAACATCTGCTGAGACTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1339
 1288 ACAGCTAGCTGAGAGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1347
 1340 TTTCTTTCGAGAGTGAATTCACAAA 1362
 1348 AGCTCTCTGTTGCCACCAAA 1370

RESULT 2
 US-09-103-840A-2/c
 ; Sequence 2, Application US/09103840A
 ; Patent No. 6294328
 ; GENERAL INFORMATION:
 ; APPLICANT: FLEISCHMAN, Robert D.
 ; APPLICANT: WHITE, Owen R.
 ; APPLICANT: FRASER, Claire M.
 ; APPLICANT: VENTER, John C.
 ; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
 ; TITLE OF INVENTION: TUBERCULOSIS
 ; FILE REFERENCE: 24366-20007.00
 ; CURRENT APPLICATION NUMBER: US/09/103,840A
 ; FILING DATE: 1998-06-24
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 4403765
 ; TYPE: DNA
 ; ORGANISM: Mycobacterium tuberculosis
 ; FEATURE:
 ; OTHER INFORMATION: CDC 1551
 ; OTHER INFORMATION: "n" bases at various positions throughout the sequence
 ; OTHER INFORMATION: represent a, t, c or g
 ; US-09-103-840A-2

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Query Match      20.6%; Score 311.2; DB 3; Length 4403765;
Best Local Similarity 54.1%; Pred. No. 1e-89;
Matches 687; Conservative 0; Mismatches 568; Indels 15; Gaps 2;

Y 80 TTCCTAGGTTCAAGATCCGCGAAACTCGATCTCTTAAGGAAGCGCGTATCAGATCATCA 139
b 3837572 TGCCGGCGCTCGGATGCCGATGAGTCGATGATCCGAGGCGGCTATCGCTTCATCC 3837513
Y 140 ACGAGGAGCTGATCTTGACGGGAATCCAGGTTGAACCTTAGCTCTTTTGACGACAT 199
b 3837512 ACGAGGAGCTGATCTTGACGGGAATCCAGGTTGAACCTTAGCTCTTTTGACGACAT 3837453
Y 200 GGATGGAGCTGAGTGTGATAAACTCATCATGCTCTCCATCAACAAGAACTATGTTGACA 259
b 3837452 GGATGGAGCTGAGTGTGATAAACTCATCATGCTCTCCATCAACAAGAACTATGTTGACA 3837393
Y 260 TGGAGGAGTACCCGTCACCAACCGAATCTCAGAACGATGTGGAACATGATGACATC 319
b 3837392 AGGACGAATACCCGCGACCGCGCCATCGAGCGGCTGTGTGTCATGCTGCGCGACC 3837333
Y 320 TATTCAATGC-----ACCGTTAGAAGGCGGAGACCGCGCTCGAGTAGGAACCG 370
b 3837332 TGTTCACGCGAGGGTCTGCGACACACGCCACCGCGCCACCGGGGTGTCCACCA 3837273
Y 371 TTGATCATCGAGGCGCATTAATGTGCGCGGTTTGGCTTCAAGCGTAAATGCGGAACA 430
b 3837272 TCGGCTCCAGCGAGGCGGTGATGCTGGGTGGCTGCGCCCTGAAATGGCGTTGGCGGCAAC 3837213
Y 431 AGCGCAAGCTGAAGGCAAAACCCGTCGATAAACCCCAACATGTGCACCGAGCCAAATGTT 490
b 3837212 GGGTGGGTCTTGAAGGGGCG-----ATGCCAATCTGGTGATGGTTGCAACGTCC 3837159
Y 491 AAGTGTGTGGGGAATATTCGCTAGGTACTTTGAGGTGAACTTAAGGAAGTGAATGCA 550
b 3837158 AGTGTGTGGGGAAGTTCTGCGCTACTTTCGACGTGCAACCCGCTTACCTGCGGATGG 3837099
Y 551 GTGAAGGATATATGTGATGAGCCCTCAACAAGCTGTGATATGTTGATGAGAACACCA 610
b 3837098 AGCGGGCGGTACGTATACACCCCGAGAGGTGCTGCGCGCGTGCAGAGAACACCA 3837039
Y 611 TTTGTGTGCGGAATCTTGTGTTTCCACTTTAATGGAANTTCGAAGATGTTAAACTCT 670
b 3837038 TCGCGCTGGTGGCATCTTGGGCAACCACTATACCGGTGAACTCGAAACCCATCGCGAGA 3836979
Y 671 TGAAGATCTCTTGTGTAAGAAACAAAGAACCGGATGGATACCAATCCAGTGG 730
b 3836978 TCTGCGCGCGCTGGACAACTGCGGCTGCGGGGTGTGAGCTCCCGTACACGTCC 3836919
Y 731 ATGCGCAAGTGGAGGATTCATGTCACCGTTTTTGTATCCGGAATGGAATGGACTTTA 790
b 3836918 ACGCGCCAGTGGGGGCTTTGTGTGCGCTTTTGCATCCGACCTGGTATGGGATTTTC 3836859
Y 791 GACTTCCCTTCGTGAAGGATCAATGTGAGTGTGTCAGATGATGCACTGTGTAGCGAG 850
b 3836858 GGCTGCCCGCGTGTGTCGATCAAGCTCAGCGCCACAAATGAGGCTGACCTATCCCG 3836799
Y 851 GGAATGTTGGGTGATCTGGAGAAACAAAGAGATTTGCCGTGAGGAACCTCATCTTCCATA 910
b 3836798 GCGTCCGGTTTGTCTGTGGCGCGGCGCCGAGACCTGCGGAGGATCTGGTTTTCCGGG 3836739
Y 911 TCATATCTTGTGCTGACCAACCGACCTTTACTCTCATTTCTCAAGGTTCAAGTTC 970
b 3836738 TCAATCTCTGCGCGGACATGCGGACCTTACCCCTGAACTTCTCCCGTCCCGGTAACC 3836679
Y 971 AAGTCATTTGCTCAATFACTACCACTTATCCGATTTGGGCCACGAGGGTTACAGAAATGCA 1030
b 3836678 AGTGTGTGGCGCAGTACTACAACTTCTGTGGCTTGGGCGCGAGCTATACCAAGTCA 3836619
Y 1031 TGGAGAAATGACAGAGATATGATCGTCTTAAGGGAAGACTTGAAGACACGAAGGT 1090
b 3836618 TGCAGCGCTGTGTCGACACCGCCCGGTGGTGGGTGACCAAGCTGCGGAGGTGATCAAT 3836559
Y 1091 TCAACATCGTCTCAAGAGGAGGAGTGCCACTTGTGCGCTTTCTCTCTTGAAGATGACA 1150
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Db 3836558 GCAGGAGTATCTCGGATGTTCCGGGATCCCGGTGTCAGCTTCCGGCTCCCGCGCAC 3836499
Qy 1151 GCTGTACACTGAGTTTGGAAATCTCCGACATGCTTCCGAGGTATGGATGGATATGCGCG 1210
Db 3836498 GCGGGTACACGAGATTCGACGCTCTCCATGAGTTCGGGACCTTCGGGTGGCAGGTGCCG 3836439
Qy 1211 CCTACCAATGCTCCAAATGCACACACATCATCTTCTCGTGTGTTATCAGAGAAG 1270
Db 3836438 CCTACCAATGCTCCGACACACCGACCTGCGGCTGCTCGGATCTGTGTTCCGGAAG 3836379
Qy 1271 ATTTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTATGCTGAGC 1330
Db 3836378 GACTTCCGCGACCTTGGCGCGGCGCTTGCACGACGCGGTCAACCGCTTGGCTGCC 3836319
Qy 1331 TCGATGAGCT 1340
Db 3836318 TGCACAAGGT 3836309

RESULT 3
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match      20.6%; Score 311.2; DB 3; Length 4411529;
Best Local Similarity 54.1%; Pred. No. 1e-89;
Matches 687; Conservative 0; Mismatches 568; Indels 15; Gaps 2;

Qy 80 TTCTTAGGTTCAAGATCCGCGAAACTCGATTCCTTAAGGAAGCGCGTATCAGATCATCA 139
Db 3851674 TGCAGCGCTGCGGATGCCCGATGATGATCCCGAGCGGCTATCGCTTCATCC 3851615
Qy 140 ACGACGAGCTGATGCTTGACGGGAATCCACGGTTGAACTTAGCTCTCTTGTGACGACAT 199
Db 3851614 ACGACGAGCTGATGCTTGACGGTAGTCTCGCGTGAATCTGGCCACCTTCGTGACCAC 3851555
Qy 200 GGATGGAGCTGAGTGTGATAAACTCATCATGCTCTCCATCAACAAGAACTATGTTGACA 259
Db 3851554 GGATGGAGCTGAGTGTGATAAACTCATCATGCTCTCCATCAACAAGAACTATGTTGACA 3851495
Qy 260 TGGACGAGTACCCCGTCCACCGAATTCAGAACCGATGTGTGAACATGATTCACATC 319
Db 3851494 AGGACGAATACCCCGGACCGCGGCTATCGGCGCTGATGTTGTCATGTTGCGCGACC 3851435
Qy 320 TATTCAATGC-----ACGTTAGAAGGCGGAGACCGCGCTGCGAGTAGGAACCG 370
Db 3851434 TGTTCACGCGGAGGCTTTCGCGACCCACCGACCCACCGCGGTGTCCACCA 3851375
Qy 371 TTGATCATCGGAGGCAATAATGTTGGCGGTTTGGCTTTCAGCGTAAATGGCAGACA 430
Db 3851374 TCGGCTCCAGAGGCGGTGATGCTGGGTGGCTGGCCCTGAAATGGCTTGGCGGCAAC 3851315
Qy 431 AGCGCAAGCTGAAGGCAAAACCCGTCGATTAACCAACCAATTTGTACCGGAGCAATGTTTC 490
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3851260 AGGTGTGTGGGAGAGTTCTCGCGTACTTTCGACGTGCAACCCCGTTACCTGCCGATGG 3851301
551 GTGAAGGATACTATGTGATGGACCTTCAACAGCTGTGTGATGTGTTGATGAGACACCA 610
3851200 AGCGGGCGCGCTACGTCATCAACCCCGAGCAGGTCTCGCCCGGTGACGAGAACACCA 3851141
611 TTTGTCTTGGGACATTTCTTGTTCCACTTTAATGAGAAATTCGAAGATGTTAAACTCT 670
3851140 TCGCGGTGTGGCGATCTTTGGGCACCACTATACCGGTGAACTCGAACCCATCGCCGAGA 3851081
671 TGAACGATCTCTGTCGAAAGAACAAAGAACCGGATGGGATACACCAATCCACGTGG 730
3851080 TCTGCCCGCGCTGGACAACTGGCGGTGGCGGGGTGTGGACGTCCCGGTACACGTGG 3851021
731 ATCGGCAAGTGGAGATTCATTGCACCGTTTTTGTATCCGAAATGGAATGGACTTTA 790
3851020 ACGCGGCAGTGGGGCTTTGTGTGCCGTTTTTGCATCCGACCTGTAIGGATTTTC 3850961
791 GACTTCCTTGTGAGAGATTCATGTGAGTGTGTCACAGTATGGACTTGTGTACGCAG 850
3850960 GGCTGCCCGCGGTGTGTCGATCAACGTGAGCGGCCACAGTATGGGTGACCTATCCCG 3850901
851 GGATTGGTGGGTGATCTCGAGAAACAAAGAGATTTTCCTGAGGAACTCATCTTCCATA 910
3850900 GCGTGGGTTGTGTCGTGGCGGGCCGAGCACCTCGCGGAGATCTGGTTTTCGGG 3850841
911 TCAATTAATCTGTGTCGTGACCAACCCACTTTTACTCTCAATTTCTCCAAAGTTTCAAGTC 970
3850840 TCAACTACTTCGCGCGGACATGCGGACCTTCACCCCTGAACCTTCTCCGTCGCCGTAAAC 3850781
971 AAGTCAATGCTCAATACTACCAACTTATCCGATTTGGGCCACGAGGTTTACAGAAATGTGA 1030
3850780 AGGTGTGGGCCAGTACTACAACTTCTGCGCTGGGCGGACGGCTATACCAAGGTGA 3850721
1031 TGGAGAAATGACAGAGATATGATGCTCTTAAGGAGAGGACTTGAAGACAGAAAGGT 1090
3850720 TGCAGGCGCTGTGCGACACCGCCCGGTGGCTGGTGACCACTGCGGAGGTGATCATTT 3850661
1091 TCAACATGCTCTCAAAGGACGAGGAGTGCCACTTGTGCTTCTCTTGAAGATAGCA 1150
3850660 GCGAGGTGATCTCGGATGTTTCGGGATCCCGGTGTCAGCTTCGGCTCCCGCGACCC 3850601
1151 GCTGTACACTGATGTTGAAATCTCGACATGCTTCGACAGTATGATGATGATGCGG 1210
3850600 GCGGGTACACGGAGTTGACAGCTTCCCATGAGCTCGGACCTTCGGGTGGCAGGTGCCG 3850541
1211 CCTACCAATGCTCCAAATGCACACACATCACTGTTCTTCTGTTGTTTATCAGAGAAG 1270
3850540 CCTACCAATGCGGACACCGCACCGAGCTGGCGGTGCTCGGATCGTGGTTCGGGAAG 3850481
1271 ATTCTCGAAGACATCGCTGAGAGACTTGTGATGATATAGAGAAATGATGCTGAGC 1330
3850480 GACTCTCCGCGACCTGGCGCGGGCCCTGCACGACGACCGGTACCCCGTGGCTGCC 3850421
1331 TCGATGAGCT 1340
3850420 TGGACAAGGT 3850411
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RESULT 4

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US-09-068-195-21
; Sequence 21, Application US/09068195B
; Patent No. 6140078
; GENERAL INFORMATION:
; APPLICANT: Sanders, Jan W.
; APPLICANT: Ledebuer, Adrianus M.
; APPLICANT: Venema, Gerard
; APPLICANT: Kok, Jan
; TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid
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; TITLE OF INVENTION: Bacterium, and Its Use in a Lactic Acid Bacterium for
; FILE OF INVENTION: Production of Desired Protein
; FILE REFERENCE: Sanders-60113/0252227
; CURRENT APPLICATION NUMBER: US/09/068,195B
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: PCT/EP97/04755
; EARLIER FILING DATE: 1997-08-20
; EARLIER APPLICATION NUMBER: EP 97200744/7
; EARLIER FILING DATE: 1997-03-13
; EARLIER APPLICATION NUMBER: EP 96202444/4
; EARLIER FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 5565
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genomic DNA of
; OTHER INFORMATION: NS3 locus containing gadRCB
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (3)..(500)
; OTHER INFORMATION: C-terminus of rnhB
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (1095)..(1922)
; OTHER INFORMATION: *ggl = gadR
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (2069)..(3577)
; OTHER INFORMATION: orfX = gadC
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (3600)..(4997)
; OTHER INFORMATION: gadB
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: Complement (15078)..(5563))
; OTHER INFORMATION: C-terminus of ORF in opposite direction
US-09-068-195-21
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Query Match 17.9%; Score 270.6; DB 3; Length 5565;
Best Local Similarity 52.4%; Pred. No. 3e-78;
Matches 678; Conservative 0; Mismatches 599; Indels 18; Gaps 3;

QY 80 TTCCTAGGTTCAAGATCCCGAAACTCGATTCCTTAAGGAAGCGGCTATCAGATCATCA 139
DB 3679 TACCTAATATTAATTAGCTCAACAATCAATTGAGCTCGAGTGGCCTATCAGTTAGTTC 3738

QY 140 ACGACGAGCTGATCTTGACGGGAATCCACGGTTGAACCTTAGCCTCTTTGTGACGACAT 199
DB 3739 AAGATGAATGCTAGATGAAGGAACGCTGTTTAAATTTGGCCACATTTCTGCAACTT 3798

QY 200 GGATGGAGCCTGAGTGTGATAAATCTCATGTCTCTCCATCAACAGAACTATGTTGACA 259
DB 3799 ATATGGAACTCTGAAGCAGTCAAGCTGATGAGTCAGACCTTGGAAGAAAATGCGATTGACA 3858

QY 260 TGGACGAGTACCCCGTCCACCACCGAACTTCAGAACCGATGTGTGAACATGATTGCACATC 319
DB 3859 AATCAGAAATATCCAAGAACCACTGAAATTTGAAACCGTTGCGTCAACATGATCGCTGACC 3918

QY 320 TATTCAATGACCGTTAGAGAGCGGAGACCGCGCTCGAGTAGGACCGTGTGATCAT 379
DB 3919 TTTGGAATGCGAGTGAAGAAA-----GGAAAAATTTATGCGGACTTCGACAAATTTGTTCTT 3972

QY 380 CGGAGGCCATAATGTTGGCCGTTTGGCCCTTCAAGCGTAAATGGCAGACAGCGCAAG 439
DB 3973 CAGAGCTTGTATGCTTGGGGGATGGCTATGAGTTTCTTGGCGTAAAGCGAGCAGAAA 4032

QY 440 CTGAAGGCAACCCGCTCGAT-----AAACCCAACTTGTACCGGAGCCAAATGTTCAAG 493
DB 4033 AATTAGGCTAGATATTAATGCGAAAAAGCCAACTTAGTCATTTCTCTGTTTATCAAG 4092
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494 TGTGTTGGAGAAATTCGCTAGGTACTTTGAGGTGAACCTTAAGGAAGTGAATGGATG 553
4093 TTTGCTGGGAAAAATTCGTGTGTTTATTGGGATATTGAATGAGAGAGTCCCAATGATA 4152
554 AAGGATACATGATGAGACCTCAACAGCTGTGTATATGTTGATGAGAACACCAATTT 613
4153 GAGACATATGTCATCAATTTGGAAAGTATGATTTGATGATATACGATTG 4212
614 GTGTTGGACATTCCTGTTGCTCACTCTTAATGAGAAATTCGAAGATGTTAACTCTTGA 673
4213 GAGTAGTTGGAATTAAGGGATTAATCTATCTGCTGCTGTTATGATGATCAAGAGCTTTGG 4272
674 ACATCTCTTGTGCGAAAGAACAAAGAACCGGATGGGATACACCAATCCAGTGGATG 733
4273 ATAAATTTGATTGAAGAAATATAATAACAGACAGACTACAAGTTTATTTACGTAGTG 4332
734 CGCAGAGTGGAGATTCATGTCACCGTTTTGTTATCCGGAAATTCGAATGGGACTTTAGAC 793
4333 CTGCTTTCAGAGGACTTTATGCTCCTTTTGTGAGCCAGAACTTGAGTGGGATTTCCGTT 4392
794 TTCCCTTGTGAGAGATCAATGATGAGTGTGTCACAGTATGGACTTTGTGTCGCGAGGA 853
4393 TGAAAAATGCTATTTCAATCAATATCTTCAGACATATAATATGTTAGTATATCCTGGTG 4452
854 TTGGTTGGTGTGTCGGAAGAACAAAGAGGATTTGCTCGAGAACTCATCTTCATATCA 913
4453 TAGGTTGGGCTTTGTGGCGTGACAAAAAATATTTACCTGAAGAGTTAATTTTAAAGTAA 4512
914 ATTATCTTGGTGTGACCAACCACTTACTCTCAATTTCTCCAAAGTTTCAAGTCAAG 973
4513 GTTAATCTGAGAGAAATTAACCAATATGCGGATTAATTTTCTCACAGTCTTCTCAAT 4572
974 TCATTCCTCAATACCACTTATTCGATTTGGCCACAGAGGTTTACAGAAATGTGATGG 1033
4573 TAATCGTCAATACTATAATTTGTACGTTATGATGATGATGATGATGATGATGATGATG 4632
1034 AGAATTCAGAGAGATATGATGCTCTTAAGGAGAGACTTGAAGACAGAAAGTTCA 1093
4633 AGAAGACGATAAAGTAGCCATGTTATTAGCAGAGAAATTAAGAAACAGAGAAATTTG 4692
1094 ACATCGTCTCAAGAGACAGGAGTGCACATTTGCTGCTTCTCTTCAAGAA-----TA 1147
4693 AGAATTAAGCATGGGACAAATTTACCAATTTGCTGCTACAAATTAAGAAATTCAA 4752
1148 GCAGCTGTCACTAGTTCGAAATCTCCGACATGCTTCGACGATGATGATGATGATGATG 1207
4753 ACCGTGTTGGAACTTTTATGATTTTGGCAGATCGTTTATTAATGAAGGATGCGAAGTC 4812
1208 CGGCTTACCAATGCTTCCAAATGCAACACATCATCTGTTCTTCTGTTGTTATCAGAG 1267
4813 CTGCTTATCCACTTCTTAAAAATTTGGAATGAAATCAATCAATCAATCAATCAATCAAT 4872
1268 AGAATTTCTGAGACACTGCTGAGAGACTTGTGATGATGATGATGATGATGATGATGATG 1327
4873 CAGATTCGGATGATATGAGCAATTAATGATGATGATGATGATGATGATGATGATGATG 4932
1328 AGCTGATGAGTCTTCTCGAGAGTGAATTCACAAA 1362
4933 CACTAAATAGGCTCATATTTCTATTTCAATCAGGAA 4967

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RESULT 5
US-08-311-731A-130/c
; Sequence 130, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311,731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 130:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36941 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LEPRAE
; US-08-311-731A-130

Query Match      8.8%; Score 133; DB 4; Length 36941;
Best Local Similarity 53.38; Pred. No. 2.3e-32;
Matches 511; Conservative 0; Mismatches 425; Indels 23; Gaps 10;

QY 93 GATCCCGGAAACTCGATTCTTAAGGAAGCGGCTATCAGATCATCAACGACGAGCTGAT 152
Db 10476 GCTGCCGAGCATCGATGGATCCTGAGCGCGGTACCGCTTTATTCACGACTAGCTAAT 10417
QY 153 GCTTGACGGAATCCACGTTTGAACCTTAGCT--CCTTTGTGACGACATGATGGAGCCT 210
Db 10416 GGTAGACGCGATTTCTCGGCTCAACCTAGGCTACTTTCTGTCACCACTGGGTGGATCCC 10357
QY 211 GAGTGTGATAAACTCATCATGTCTCTCATCAACAGAACTATGTTGACATGACGAGTAC 270
Db 10356 GAGGTAAAGAGTTTGATGGCGCGAGACGTTTCGACAAACATGTTTAGACAAGGACGAGTAT 10297
QY 271 CCCGTCACCCAGAACTTCAGAACCGATGTTGAAACATGATTCACATCTATTTCATGCA 330
Db 10296 CCGG---CGGCGCGCCATCGAACGCGCTGCGTATAGCATGCGACCGGTCTCTATTCA 10240
QY 331 CCGTTAGAAAGGCGGAGACCGCGTCCGAGTAGGAACCGTTGGATCATCGGAGGCCATA 390
Db 10239 GCGCTAG--GGACTCAGCTACGACAAACCGCTCAATACCTGTGGGGTGTCCATTATCGGC 10181
QY 391 ATGTTGGCGGTTTGGCTTCAAGCGTAAATGGCAAGCAAGCGCAAGCTGAAGGCABA 450
Db 10180 TCCAGGGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 10121
QY 451 CCCGT-----CGATAAAACCCAACTTGTACCAGGAGCAATGTTCAAGTGTGTGGG 502
Db 10120 CTAGTTAGCAGCGTAGCACCCCAATCTGGGGATGGCGCAGGGGTCCAGGTGGTTGGG 10061
QY 503 AGAATTCGCTAGTACTTTGAGTTGAACTTAAGNAGTGAATTCAGTGAAGTACT 562
Db 10060 AGAAGTTCTGTGTTACTTCTGATGTCAGC--CGCTATCTGTGATGGAGGAGGATGCT 10003
QY 563 ATGTGATGAGCCCTCAACAAAGCTGTTGATATG--GTTGATGAGAACACCAATTTGTGTTGC 620

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10002 AGCTCATACCTCCGAGAGAGTAATCGAGGCCGCTGACGAGGACACTACTTGGTGTG 9943
621 GGACATCTTGTGT--TCCACTCTTAATGGAGAATTGGAAGATGTTAAACTCTTTGAACGAT 678
9942 TGGCCATCTTTGCTGCCACTTTCACCGGGAACTCGAACCCGTCGGGAGCTCTGGTC 9883
679 CTTCTGGTGAAGAACAACAAGAACCGATGGATACACCAATCCACGTTGGATGGGCA 738
9882 GCGCTGGAACAGCTGGACCCGACAAATGGCTTGGACATTTGCAGTGTCCGTCGGTCCGCC 9823
739 AGTGAAGATTCATTGCAACCGCTTTTGTATCCGAATTGGAATGGAGCTTTTAGACTTCCC 798
9822 AGCGG-GGGTTCCGGATGCCITGCTTGACCGGAGTTGAAGTGGATCTCTGCTGCC 9764
799 TTGGTGAAGAGTATCATAGT-GAGTGGTCACAAGTATGGACT-TGTGTACGAGGGATTG 856
9763 CGAGTGATGTCATCAATGTAAGTGGCTATAAATATGGGCTCACCCCTACCCCGGTTGG 9704
857 GTTGGTGATCTGGAGAAACAAGAGGATTTGCCCTGAGGAATCATCTTCCATATCAATT 916
9703 GATTGGCGTATGGCGGCAACGAATATTTGCCGAGGACGTAGTCTTTGCTGCACT 9644
917 ATCTTGGTCTGACCAACCCACTTTACTCTCAATTTCTCCAAAGTTCAAGTCAAGTCA 976
9643 ACTCGGGCGGCGATATGTAGACTTTTCGTAATGAACCTTTTCCCGCTGGACAACCAAGTG 9584
977 TTGCTCAATCACTACCAACTTATCCGATTTGGCCACGAGGGTTACAGAAATGTGTAGAG 1035
9583 TTAGTCAGTACTACAACCTTCTGTGGCTGGACGTACGGTTACTGGAAGTATGTCAG 9525

RESULT 6

S-09-056-556-192/c
Sequence 192, Application US/09056556
Patent No. 6350456

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 192:

SEQUENCE CHARACTERISTICS:
LENGTH: 359 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-056-556-192

TREATM

Query Match 4.2%; Score 64; DB 4; Length 359;
Best Local Similarity 58.3%; Pred. No. 5.9e-11;
Matches 112; Conservative 0; Mismatches 80; Indels 0; Gaps 0;
QY 844 TACGACGAGGATTGGTTGGGTGATCTGGAGAAACAAGAGGATTTGGCTGAGGAACCTCATC 903
Db 353 TATCCGCGCTCGGGTTTGTGCTGTGGCGGGCCGAGCACTGCGGAGGATCTGGTT 294
QY 904 TTCAATATCAATATCTTGGTGTGCTGACCAACCACTTTACTCTCAATTTCTCCAAAGT 963
Db 293 TTCCGGGTCAACTACCTCGCGCGGACATGCCGACCTTCACCTGAACTTCTCCGTC 234
QY 964 TCAAGTCAAGTCATTGTCTCAATCACTCAACTTATCCGATTTGGGCCACGAGGTTACAGA 1023
Db 233 GGTAAACAGGTGGTGGCCAGTACTCAACTTCTCGGCTGGGGCGGACGCTATACC 174
QY 1024 AATGTATGGAG 1035
Db 173 AAGGTATGCAG 162

RESULT 7

US-09-072-596-187/c
Sequence 187, Application US/09072596
Patent No. 6458366

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Twardzik, Thomas S.
APPLICANT: Lodes, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 187:

SEQUENCE CHARACTERISTICS:
LENGTH: 359 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-072-596-187

Query Match 4.2%; Score 64; DB 4; Length 359;
Best Local Similarity 58.3%; Pred. No. 5.9e-11;
Matches 112; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 844 TACGACGAGGATTGGTTGGGTGATCTGGAGAAACAAGAGGATTTGGCTGAGGAACCTCATC 903

NAME/KEY: misc feature	LOCATION: (510001)..(525000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (525001)..(540000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (540001)..(555000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (555001)..(570000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (570001)..(585000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (585001)..(600000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (600001)..(615000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (615001)..(630000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (630001)..(645000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (645001)..(660000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (660001)..(675000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (675001)..(690000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (690001)..(705000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (705001)..(720000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (720001)..(735000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (735001)..(750000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (750001)..(765000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (765001)..(780000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (780001)..(795000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (795001)..(810000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (810001)..(825000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (825001)..(840000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (840001)..(855000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (855001)..(870000)	OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature	LOCATION: (870001)..(885000)	OTHER INFORMATION: n=a or c or g or t

OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (885001)..(900000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (900001)..(915000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature

Query Match 2.6%; Score 39.2; DB 4; Length 1230025;
Best Local Similarity 51.1%; Pred. No. 1.8; Indels 0; Gaps 0;
Matches 92; Conservative 0; Mismatches 88;
Y 523 GAGGTGAACCTTAAGAGAGTGAATGAGTCAAGGACTATGATGGAGCCCTCAACAA 582
b 784726 GAAATTTAGATACCTTCAAAAATAGTATACCTTTAGATGAGCAGAGCGCTTACTA 784667
Y 583 GCTGTTGATATGGTTGATGAGAACACCACTTTGTTGCGGACATCTTTGGTTCACCTTT 642
b 784666 AATGTCGAGAATGTTGCTGTAGATTAGTTTGGACTCGGTCTCTATTGGAACCACTTT 784607
Y 643 AATGAGAAATTCGAAGATGTTAACTCTTGAACGATCTTTGGTGGAAAAGAACAAAGAA 702
b 784606 AAGAAGCGTTGAAAAGCCCGAGTATTTCTGTTCTTTGGCGAGCGATTCAAGAA 784547

RESULT 10
S-08-781-891-208/c
Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-1996

Query Match 2.4%; Score 35.8; DB 3; Length 16442;
Best Local Similarity 56.3%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 52;
Y 933 ACCGACCTTTACTCTCAATTTCTCCAAAGGTTCAAGTCAATGCTCAATACTACCA 992
b 207 ACCCAACCAAACTCTCAATTTCCCATAGTGGAGAAACAAGTATTTCCATGACAATACCA 148
Y 993 ACTTATCCGATTGGGCCACGAGGTTTACAGAAATGTGATGGAGAAATTCGACAGAGAATA 1051
b 147 AATTCACACATTATCTCTCCAGGATCCAGCCCTTCAAGAGATAATAACAGAAAAAAA 89

RESULT 12
US-08-781-891-208
Sequence 208, Application US/08781891
Patent No. 6090620
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,891
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-1996

Query Match 2.4%; Score 35.8; DB 3; Length 16442;
Best Local Similarity 56.3%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 52;
Y 933 ACCGACCTTTACTCTCAATTTCTCCAAAGGTTCAAGTCAATGCTCAATACTACCA 992
b 207 ACCCAACCAAACTCTCAATTTCCCATAGTGGAGAAACAAGTATTTCCATGACAATACCA 148
Y 993 ACTTATCCGATTGGGCCACGAGGTTTACAGAAATGTGATGGAGAAATTCGACAGAGAATA 1051
b 147 AATTCACACATTATCTCTCCAGGATCCAGCCCTTCAAGAGATAATAACAGAAAAAAA 89

QY 933 ACCGACCTTTACTCTCAATTTCTCCAAAGGTTCAAGTCAATGCTCAATACTACCA 992
DB 207 ACCCAACCAAACTCTCAATTTCCCATAGTGGAGAAACAAGTATTTCCATGACAATACCA 148
QY 993 ACTTATCCGATTGGGCCACGAGGTTTACAGAAATGTGATGGAGAAATTCGACAGAGAATA 1051
DB 147 AATTCACACATTATCTCTCCAGGATCCAGCCCTTCAAGAGATAATAACAGAAAAAAA 89

RESULT 11
US-09-618-166-208/c
Sequence 208, Application US/09618166
Patent No. 6583112
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/618,166
FILING DATE: 17-Jul-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 240052.419C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 208:
US-09-618-166-208

Query Match 2.4%; Score 35.8; DB 4; Length 16442;
Best Local Similarity 56.3%; Pred. No. 1.4; Indels 0; Gaps 0;
Matches 67; Conservative 0; Mismatches 52;
QY 933 ACCGACCTTTACTCTCAATTTCTCCAAAGGTTCAAGTCAATGCTCAATACTACCA 992
DB 207 ACCCAACCAAACTCTCAATTTCCCATAGTGGAGAAACAAGTATTTCCATGACAATACCA 148
QY 993 ACTTATCCGATTGGGCCACGAGGTTTACAGAAATGTGATGGAGAAATTCGACAGAGAATA 1051
DB 147 AATTCACACATTATCTCTCCAGGATCCAGCCCTTCAAGAGATAATAACAGAAAAAAA 89

RESULT 12
US-09-601-198-60/c
Sequence 60, Application US/09601198
Patent No. 6531583
GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TO
TITLE OF INVENTION: WERNER'S SYNDROME
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/601,198
FILING DATE: 27-DEC-1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: No. 6090620tenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 240052.419
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-1996

APPLICANT: Cassell, Gail H.
 APPLICANT: Chen, Ellison Y.
 APPLICANT: Glass, Jennifer S.
 APPLICANT: Glass, John I.
 APPLICANT: Heiner, Cheryl R.
 APPLICANT: Lefkowitz, Elliot
 TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
 TITLE OF INVENTION: UREALYTICUM
 FILE REFERENCE: UAB-13452/22
 CURRENT APPLICATION NUMBER: US/09/601,198
 PRIOR FILING DATE: 2000-12-08
 PRIOR APPLICATION NUMBER: 60/073,189
 PRIOR FILING DATE: 1998-01-30
 NUMBER OF SEQ ID NOS: 181
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 60
 LENGTH: 15016
 TYPE: DNA
 ORGANISM: Ureaplasma urealyticum
 5-09-601-198-60

 Query Match 2.4%; Score 35.6; DB 4; Length 15016;
 Best Local Similarity 47.7%; Pred. No. 1.6; Indels 0; Gaps 0;
 Matches 104; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

 Y 461 AACCCAACTTGTCCACCGAGCCCAATGTTCAAGTGTGTTGGGAGAAATTCGCTAGGTACT 520
 b 9593 AACTAAATTTGCTATCAATGATTTTGAAGGATGTTTAAAGGAAATCAAACTTTAAGT 9534
 Y 521 TTGAGTTGAACCTTAAGGAAGTGAATGAGTGAAGTACTATGATGACCCCTCAAC 580
 b 9533 TTAATATCAACCAATGAAATGAGTGTGCTAATTTAAATGAGATTGCGAACATGAAG 9474
 Y 581 AAGCTGTTGATATGTTGATGAGAACCAATTTGTTGTTGGGACATCTTGTGTTCCACTC 640
 b 9473 GTAAAGTAGAATATTGATGCGCAAAATTTCTTTGTTGCTAATCTTAATAACATTAAAG 9414
 Y 641 TTAATGGGAATTCGAAGATGTTAACTCTTGAACGAT 678
 b 9413 TTAACAAAGATATAAAGTTTATAAATCTACTTTGAT 9376

 RESULT 13
 US-09-026-408-11/5
 Sequence 11, Application US/09026408
 Patent No. 6303338
 GENERAL INFORMATION:
 APPLICANT: Ni et al.
 TITLE OF INVENTION: PANCREAS-DERIVED PLASMINOGEN ACTIVATOR
 TITLE OF INVENTION: INHIBITOR
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 STREET: 1100 NEW YORK AVENUE, SUITE 600
 CITY: WASHINGTON
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/026,408
 FILING DATE: Herewith
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/934,011
 FILING DATE: 15-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/024,056
 FILING DATE: 16-AUG-1996

ATTORNEY/AGENT INFORMATION:
 NAME: STEFFE, ERIC K.
 REGISTRATION NUMBER: 36,688
 REFERENCE/DOCKET NUMBER: 1488.0300002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-371-2600
 TELEFAX: 202-371-2540
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 515 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 US-09-026-408-11

 Query Match 2.2%; Score 33.6; DB 4; Length 515;
 Best Local Similarity 50.0%; Pred. No. 0.78; Indels 0; Gaps 0;
 Matches 81; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

 QY 525 GGTGAACCTTAAGGAAGTGAATTTGAGTGAAGGATACTATGTGATGACCCCTCAACAAGC 584
 Db 506 GGTATGTTCAAGNATCCAAACGTCCTTTGGAGTCTACTTTTGGTCTCTACTTTAATCTGGT 447
 QY 585 TGTGATATGTTGATGAGAACACCATTTGTTGCGGACATCTTGGTTCCTCACTTTAA 644
 Db 446 ATTNAAAAAAAGAAAGAAAGTCTTGAACACATGTCACATTTTGTCTACCAATTTT 387
 QY 645 TGGAGAATTCGAAGATGTTAAACCTCTTTGAACGATCTCTTGGT 686
 Db 386 AATGATGACTTAGAGGATAATAATTGTAANAATCTTTTGGT 345

 RESULT 14
 US-08-471-033-18
 Sequence 18, Application US/08471033
 Patent No. 5770696
 GENERAL INFORMATION:
 APPLICANT: Warren, Gregory W
 APPLICANT: Kozziel, Michael G
 APPLICANT: Mullins, Martha A
 APPLICANT: Nye, Gordon J
 APPLICANT: Carr, Brian
 APPLICANT: Desai, Nalini M
 APPLICANT: Kostichka, N. Kristy
 APPLICANT: Duck, Nicholas B
 APPLICANT: Estruch, Juan J
 TITLE OF INVENTION: No. 5770696e1 Pesticidal Proteins and Strains
 NUMBER OF SEQUENCES: 50
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: NY
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/471,033
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/314,594
 FILING DATE: 09-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/218,018
 FILING DATE: 23-MAR-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/037,057

FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV7 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2004 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2004
OTHER INFORMATION: /note= "Maize optimized DNA
OTHER INFORMATION: sequence for VIPIA(a) 80 kd protein from AB78"
3-08-471-033-18

Query Match 2.2%; Score 33.4; DB 1; Length 2004;
Best Local Similarity 55.7%; Pred. NO. 2.2;
Matches 64; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Y 1375 CAAGAGAGAGTGAATCTACACGCGATATCATCTGATGGTGAAGAGCGGATATC 1434
b 1357 CAGGAGAGCTGACACAGACCGGACTACTACATCAGCTGTACATGAAGAGCGGAG 1416

Y 1435 GACAAGCAGAGAGATATCATCTGCTGGAGAGAGTTTGTCCCGACAGGAAGA 1489
b 1417 AACACCCAGTGGAGATCACCATCGACGGCGAGATATACCCCATCACCACCAAGA 1471

RESULT 15
S-08-471-044-18
Sequence 18, Application US/08471044
Patent No. 5840868
GENERAL INFORMATION:
APPLICANT: Warren, Gregory W
APPLICANT: Koziel, Michael G
APPLICANT: Mullins, Martha A
APPLICANT: Nye, Gordon J
APPLICANT: Carr, Brian
APPLICANT: Desai, Nalini M
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESS: CIBA-GEIGY Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,044
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/218,018
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CGC 1695/CIP3/DIV6 - SOLV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 2004 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:
NAME/KEY: misc feature
LOCATION: 1..2004
OTHER INFORMATION: /note= "Maize optimized DNA
OTHER INFORMATION: sequence for VIPIA(a) 80 kd protein from AB78"
US-08-471-044-18

Query Match 2.2%; Score 33.4; DB 2; Length 2004;
Best Local Similarity 55.7%; Pred. NO. 2.2;
Matches 64; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 1375 CAAGAGAGAGTGAATCTACACGCGATATCTTGTGTCACCGTGAAGAGAGCGGATATC 1434
DB 1357 CAGGAGAGCTGACACAGACCGGACTACTACATCAGCTGTACATGAAGAGCGGAG 1416

QY 1435 GACAAGCAGAGAGATATCATCTGCTGGAGAGAGTTTGTCCCGACAGGAAGA 1489
DB 1417 AACACCCAGTGGAGATCACCATCGACGGCGAGATATACCCCATCACCACCAAGA 1471

Search completed: October 22, 2003, 13:36:58
Job time : 133 secs

WPI: 2002-490073/52.
P-PSDB; AAO15132.

Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome

Claim 18; Page 53; 63pp; English.

The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAD), to provide a transformed plant that expresses the GAD coding sequence in response to a signal. Plants of this type have an enhanced ability to tolerate environmental or other stresses. The present sequence is the A. thaliana GAD1 coding sequence.

Sequence 1509 BP; 433 A; 321 C; 385 G; 370 T; 0 other;

Query Match 100.08; Score 1509; DB 24; Length 1509;

Best Local Similarity 100.08; Pred. No. 0;

Matches 1509; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

y	1	ATGTTGCTCTCCACGGCGTATCGAGTTCGGAGTTCGGTCCACATCCACATTCGCATCA	60
b	1	ATGTTGCTCTCCACGGCGTATCGAGTTCGGAGTTCGGTCCACATCCACATTCGCATCA	60
y	61	CGTTAGTCCGTACTTCTCTCTAGTTTCTAGATTCGAGTTCGGTCCACATTCGCATCA	120
b	61	CGTTAGTCCGTACTTCTCTCTAGTTTCTAGATTCGAGTTCGGTCCACATTCGCATCA	120
y	121	CGGGGTATCAGATCATCAACGACGAGTCTGCTTCACGGGAATCCACGGTTCGAATTA	180
b	121	CGGGGTATCAGATCATCAACGACGAGTCTGCTTCACGGGAATCCACGGTTCGAATTA	180
y	181	GCCTCTTTGTGACATGATGAGTCTGAGTGTGATTAATCATCATGCTCTCTGATC	240
b	181	GCCTCTTTGTGACATGATGAGTCTGAGTGTGATTAATCATCATGCTCTCTGATC	240
y	241	AACAAAGTATGTTGATGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT	300
b	241	AACAAAGTATGTTGATGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT	300
y	301	GTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360
b	301	GTGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	360
y	361	GTAGAACCGTTGGATCATCGAGGCGCATATGTTGGCGGTTTGGCGTTTCAAGCGTAA	420
b	361	GTAGAACCGTTGGATCATCGAGGCGCATATGTTGGCGGTTTGGCGTTTCAAGCGTAA	420
y	421	TGGCAGAACGCGCAAGCTGAAGCGCAACCGGTTCGATTAACCCCAATTTGTCACCGGA	480
b	421	TGGCAGAACGCGCAAGCTGAAGCGCAACCGGTTCGATTAACCCCAATTTGTCACCGGA	480
y	481	GCCATGTTCAAGTGTGTTGGAGAAATTCGTAGTACTTTGAGGTTGAACTTAAGGAA	540
b	481	GCCATGTTCAAGTGTGTTGGAGAAATTCGTAGTACTTTGAGGTTGAACTTAAGGAA	540
y	541	GTGAATGAGTGAAGGATCTATCTGATGAGTCTCAACAGCTGTTGATGATGATGAT	600
b	541	GTGAATGAGTGAAGGATCTATCTGATGAGTCTCAACAGCTGTTGATGATGATGAT	600
y	601	GAGAACCATTTGTTGTCGGACATTTCTGTTCCACTCTTAATGAGAAATTCGAAGAT	660
b	601	GAGAACCATTTGTTGTCGGACATTTCTGTTCCACTCTTAATGAGAAATTCGAAGAT	660
y	661	GTTAACTCTTGAACCGATCTCTTGGTGAAGAAACAAAGAGATTTGCTGAGGAACTC	720
b	661	GTTAACTCTTGAACCGATCTCTTGGTGAAGAAACAAAGAGATTTGCTGAGGAACTC	720

Db	661	GTTAACTCTTGAACCGATCTCTTGGTGAAGAAACAAAGAGATTTGCTGAGGAACTC	720
Qy	721	ATCCACGTGATCGGCAAGTGGAGGATTCATTCGACCGTTTGTATCCGGAATGGAA	780
Db	721	ATCCACGTGATCGGCAAGTGGAGGATTCATTCGACCGTTTGTATCCGGAATGGAA	780
Qy	781	TGGGACTTTAGACTTCCCTTGGTGAAGAGATCAATCTGAGTGGTCAAGTATGAGCTT	840
Db	781	TGGGACTTTAGACTTCCCTTGGTGAAGAGATCAATCTGAGTGGTCAAGTATGAGCTT	840
Qy	841	GTGTACCGAGGATTTGGTGGTGAATTCGAGAAACAAAGAGATTTGCTGAGGAACTC	900
Db	841	GTGTACCGAGGATTTGGTGGTGAATTCGAGAAACAAAGAGATTTGCTGAGGAACTC	900
Qy	901	ATCTTCCATATCAATATCTTGGTGGTGAACCAACCCACCTTACTCTCAATTTCTCCAA	960
Db	901	ATCTTCCATATCAATATCTTGGTGGTGAACCAACCCACCTTACTCTCAATTTCTCCAA	960
Qy	961	GTTTCAAGTCAAGTCAATGCTCAATCTACCACTTATCCGATTCGAGTGGCCACGAGGTTAC	1020
Db	961	GTTTCAAGTCAAGTCAATGCTCAATCTACCACTTATCCGATTCGAGTGGCCACGAGGTTAC	1020
Qy	1021	AGAAATGTGATGAGAAATTCGAGAGAAATATGATCGTCTTAAGGAAAGACTTGAGAAG	1080
Db	1021	AGAAATGTGATGAGAAATTCGAGAGAAATATGATCGTCTTAAGGAAAGACTTGAGAAG	1080
Qy	1081	ACAGAAAGTTCAACATCTGCTCAAGGACGAGGAGTGCACCTTGTCTCTCTCTCTG	1140
Db	1081	ACAGAAAGTTCAACATCTGCTCAAGGACGAGGAGTGCACCTTGTCTCTCTCTCTG	1140
Qy	1141	AAAGATGACGCTGTCACATCTGAGTTCGAAATCTCCGACATGCTTCGAGGATGATGATG	1200
Db	1141	AAAGATGACGCTGTCACATCTGAGTTCGAAATCTCCGACATGCTTCGAGGATGATGATG	1200
Qy	1201	ATAGTCCGGGCTACACAATCGCTCCAAATGCAACACATCATCTGTTCTGTTGGTT	1260
Db	1201	ATAGTCCGGGCTACACAATCGCTCCAAATGCAACACATCATCTGTTCTGTTGGTT	1260
Qy	1261	ATCAGAGAGATTTCTCGAAGCACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG	1320
Db	1261	ATCAGAGAGATTTCTCGAAGCACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG	1320
Qy	1321	ATGCGTGAAGTTCGATGAGTCTTCTCGAGAGTCAATTCACAAATATACATTCGACAAAG	1380
Db	1321	ATGCGTGAAGTTCGATGAGTCTTCTCGAGAGTCAATTCACAAATATACATTCGACAAAG	1380
Qy	1381	AAGAGTGAATCTAACAGCGATACTTCACTGATGATGATGATGATGATGATGATGATG	1440
Db	1381	AAGAGTGAATCTAACAGCGATACTTCACTGATGATGATGATGATGATGATGATGATG	1440
Qy	1441	CAGAGAGATATCATCATCTGCTGGAAGAAAGTTTGTCCGCCACAGGAAGAGACGAGTGT	1500
Db	1441	CAGAGAGATATCATCATCTGCTGGAAGAAAGTTTGTCCGCCACAGGAAGAGACGAGTGT	1500
Qy	1501	ATCTGCTTAA 1509	
Db	1501	ATCTGCTTAA 1509	

RESULT 2

ABZ14005

ID ABZ14005 standard; DNA; 1509 BP.

XX ABZ14005;

XX AC ABZ14005;

XX 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 1810.

XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

XX Arabidopsis thaliana.

1 WO200216655-A2.
2
3 28-FEB-2002.
4
5 24-AUG-2001; 2001WO-US26685.
6
7 24-AUG-2000; 2000US-227866P.
8 26-JAN-2001; 2001US-264647P.
9 22-JUN-2001; 2001US-300111P.
10
11 (SCRI) SCRIPTS RES INST.
12 (SYGN) SYNGENTA PARTICIPATIONS AG.
13 Harper JF, Kreps J, Wang X, Zhu T;
14
15 WPI; 2002-304127/34.
16
17 Identifying a stress condition to which a plant cell has been exposed
18 and producing plants with increased tolerance to these abiotic stresses
19
20
21 Claim 144; SEQ ID NO 1810; 577pp + Sequence Listing; English.
22
23 The invention relates to identifying a stress condition to which a plant
24 cell has been exposed, comprising:
25 (a) contacting nucleic acid representative of expressed polynucleotides
26 in the plant cell with an array or probes representative of the plant
27 cell genome; and
28 (b) detecting a profile of expressed polynucleotides in the plant cell
29 characteristic of a stress response. The method is useful in the
30 production of transgenic plants, cells and seeds and in producing plants
31 with increased tolerance to abiotic stress. The present sequence is that
32 of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
33 in methods of the invention.
34 Note: The sequence data for this patent is not represented in the printed
35 specification but is based on sequence information supplied to Derwent by
36 the European Patent Office.
37
38 Sequence 1509 BP; 432 C; 322 C; 385 G; 370 T; 0 other;
39
40 Query Match 99.9%; Score 1507.4; DB 24; Length 1509;
41 Best Local Similarity 99.9%; Pred. No. 0;
42 Matches 1508; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
43
44 1 ATGGGCTCTCCACGCGTATCGAGTCGAGCTCTCCGTCACCTCCACATTCGATCA 60
45 1 ATGGGCTCTCCACGCGGATTCGAGTCGAGCTCTCCGTCACCTCCACATTCGATCA 60
46
47 61 GGTACGTCCTTACTTCACTTCTCCTAGGTTCAAGATGCGGAAATCTCGATTCTTAAGGAA 120
48 61 GGTACGTCCTTACTTCACTTCTCCTAGGTTCAAGATGCGGAAATCTCGATTCTTAAGGAA 120
49
50 121 GCGGCGTATCAGATCAATCAACGAGCTGATGCTGACGCGGAAATCCACGTTGAACCTTA 180
51 121 GCGGCGTATCAGATCAATCAACGAGCTGATGCTGACGCGGAAATCCACGTTGAACCTTA 180
52
53 181 GCTCCTTTTGTGACACATGATGAGCTGAGCTGATGATGATGATGATGATGATGATGATG 240
54 181 GCTCCTTTTGTGACACATGATGAGCTGAGCTGATGATGATGATGATGATGATGATGATG 240
55
56 241 AACAAAGAACTATGTTGACATGGAATGACATGACATGACATGACATGACATGACATGAC 300
57 241 AACAAAGAACTATGTTGACATGGAATGACATGACATGACATGACATGACATGACATGAC 300
58
59 301 GTGACATGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
60 301 GTGACATGATGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
61
62 361 GTAGGAAACCGTTGGATCATCGGAGGCGGATGATGATGATGATGATGATGATGATGATG 420
63 361 GTAGGAAACCGTTGGATCATCGGAGGCGGATGATGATGATGATGATGATGATGATGATG 420
64
65 421 TGGCAGAAACGCGGAAAGCTGAAGGCAACCCGTCGATTAACCCCAACATTTGTCACCGGA 480

421 TGGCAGAAACGCGGAAAGCTGAAGGCAACCCGTCGATTAACCCCAACATTTGTCACCGGA 480
481 GCCAATGTTCAAGTGTGTTGGGAGAAATTCCTAGGTACTTTGAGGTGAACTTAAGGAA 540
481 GCCAATGTTCAAGTGTGTTGGGAGAAATTCCTAGGTACTTTGAGGTGAACTTAAGGAA 540
541 GTGAAATTTGAGTGAAGGATACTATGTGATGACCCCTCAACAAGCTGTTGATATGGTTGAT 600
541 GTGAAATTTGAGTGAAGGATACTATGTGATGACCCCTCAACAAGCTGTTGATATGGTTGAT 600
601 GAGAACACCATTTGTTGGGCAATTCCTTGGTCCACTCTTAATGAGAAATTCGAAGAT 660
601 GAGAACACCATTTGTTGGGCAATTCCTTGGTCCACTCTTAATGAGAAATTCGAAGAT 660
661 GTTAAACTCTTGAACGATCTCTTGGTCGAAAGAAACAAAGAAACCCGATGGGATACACCA 720
661 GTTAAACTCTTGAACGATCTCTTGGTCGAAAGAAACAAAGAAACCCGATGGGATACACCA 720
721 ATCCACGTGATGCGGCAAGTGGAGGATTCATTGCAACCGCTTTTGTATCCGGAATTCGAA 780
721 ATCCACGTGATGCGGCAAGTGGAGGATTCATTGCAACCGCTTTTGTATCCGGAATTCGAA 780
781 TGGACTTTAGACTTCCCTTGGTCAAGAGTATCAATGTGAGTGGTCAAGTATGACAT 840
781 TGGACTTTAGACTTCCCTTGGTCAAGAGTATCAATGTGAGTGGTCAAGTATGACAT 840
841 GTGTACGCGAGGATTTGGTGGTGATCTGGAGAAACAAAGAGGATTTGCCCTGAGGAATC 900
841 GTGTACGCGAGGATTTGGTGGTGATCTGGAGAAACAAAGAGGATTTGCCCTGAGGAATC 900
901 ATCTTCATATCAATATCTTGGTGGTGATCAACCCGCTTTTACTCTCAATTTCTCAAA 960
901 ATCTTCATATCAATATCTTGGTGGTGATCAACCCGCTTTTACTCTCAATTTCTCAAA 960
961 GGTTCAGTCAAGTCAATGCTCAATATCTCAACCTTATCCGATTTGGCCACAGGGTTAC 1020
961 GGTTCAGTCAAGTCAATGCTCAATATCTCAACCTTATCCGATTTGGCCACAGGGTTAC 1020
1021 AGAATGTGATGGAGAAATGCGAGAGAAATATGATGCTCTTAAGGGAAGGATTTGAGAAG 1080
1021 AGAATGTGATGGAGAAATGCGAGAGAAATATGATGCTCTTAAGGGAAGGATTTGAGAAG 1080
1081 ACAGAAAGTTCAACATGCTCTCAAGAGAGGAGTGCACCTTGCCTTTCTCCTTG 1140
1081 ACAGAAAGTTCAACATGCTCTCAAGAGAGGAGTGCACCTTGCCTTTCTCCTTG 1140
1141 AAAGATAGCAGCTGTCACACTGAGTTTCAAAATCTCCGACATGCTTCGAGGTATGATGG 1200
1141 AAAGATAGCAGCTGTCACACTGAGTTTCAAAATCTCCGACATGCTTCGAGGTATGATGG 1200
1201 ATAGTCCGCGCTACCAATGCTTCCAAATGCAACACATCACTGTTCTTCTGTTGGTT 1260
1201 ATAGTCCGCGCTACCAATGCTTCCAAATGCAACACATCACTGTTCTTCTGTTGGTT 1260
1261 ATCAGAGAAAGTTTCTCGAGAACTCTGCTGAGAGCTTGTGATCGATATAGAGAAAGTG 1320
1261 ATCAGAGAAAGTTTCTCGAGAACTCTGCTGAGAGCTTGTGATCGATATAGAGAAAGTG 1320
1321 ATGCGTGAAGTCAATGAGTTCCTTTCGAGAGTGAATTCACAAATATCACTTGGCAAGAG 1380
1321 ATGCGTGAAGTCAATGAGTTCCTTTCGAGAGTGAATTCACAAATATCACTTGGCAAGAG 1380
1381 AAGAGTGAATCTAAGAGGATATCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1440
1381 AAGAGTGAATCTAAGAGGATATCTTGTGATGATGATGATGATGATGATGATGATGATGAT 1440
1441 CAGAGAGATATCACTACCTGGCTGGAAGAGTTTGTGCGCCGACAGGAGAGAGAGAGTGGT 1500
1441 CAGAGAGATATCACTACCTGGCTGGAAGAGTTTGTGCGCCGACAGGAGAGAGAGAGTGGT 1500
1501 ATCTGCTTAA 1509
1501 ATCTGCTTAA 1509

1331 ATTAGAGAGATTCTCCGGTACACTCGCCGAGCGACTGTAATAGACATTGAAAAGTC 1390
 1321 ATGCGTGAGCTCGATGAGCTTCCCTTCAGAGTGATTCACAAAATATCATCTTGGACAAAGAG 1380
 1391 CTCCACGAGCTAGACACACTTCCGGCGAGGGTCAACGCTAAGCTAGCCGTCGGCGAGGCG 1450
 1381 AAGAGTGAATCTAACACGAGGATACTTGTATGCTCAGGCTGAAGAGAGCGATATCGACAAAG 1440
 1451 AATGG-----CAGCGGCTGCATPAGAAAACAGATAGAGAGTG 1489
 1441 CAGAGAGATATCATCACTGCTGGAAGAACTTTGTCCGACAGGAGAGAGAGCT 1497
 1490 CAGCTTGAGATTACTACTGATGAGAGAAATTTGTTGCTGATAGAGAGAGAGACT 1546

RESULT 4
 AAL43417 standard; DNA; 1784 BP.
 AAL43417;
 25-SEP-2002 (first entry)
 Petunia GAD coding sequence.
 GAD; plant GABA production regulation; glutamic acid decarboxylase;
 plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ds.
 Petunia sp.
 WO200238736-A2.
 16-MAY-2002.
 07-NOV-2001; 2001WO-US47447.
 07-NOV-2000; 2000US-246367P.
 (EMER-) EMERALD BIOAGRICULTURE CORP.
 Kinnersley AM, Turano PJ;
 WPI: 2002-490073/52.
 P-PSDB; AAO15139.
 Making transformed plants that selectively increase gamma-aminobutyric
 acid production, by incorporating a DNA construct with a polynucleotide
 encoding a plant glutamic acid decarboxylase enzyme into plant's genome
 -
 Claim 18; Page 58; 63pp; English.

The present invention relates to a method of producing a transformed
 plant that selectively increases production of gamma-aminobutyric acid
 (GABA) in response to a signal, by incorporating into the plant's genome
 a DNA construct with a non-constitutive promoter operably linked to a
 polynucleotide encoding a functional plant glutamic acid decarboxylase
 (GAD), to provide a transformed plant that expresses the GAD coding
 sequence in response to a signal. Plants of this type have an enhanced
 ability to tolerate environmental or other stresses. The present sequence
 is the petunia GAD coding sequence.

Sequence 1784 BP; 550 A; 298 C; 400 G; 536 T; 0 other;
 Query Match 57.7%; Score 871.4; DB 24; Length 1784;
 Best Local Similarity 74.9%; Pred. No. 7.4e-257;
 Matches 1121; Conservative 0; Mismatches 366; Indels 10; Gaps 2;

1 ATGGGTGCTCCACGCGCGTATCGAGTGGAGCGCTCCGTCACACTCCACATTCGCATCA 60
 72 ATGGTCTATCAAGACAGTGTCCGAGAGCGATGTGTCATTCCTCCAGTTTGCTTCT 131

QY 61 CGTTACCTCGGTACTTCACTTCTAGTCTCAAGATCCCGAAAACTCGATTCTCTAAGGAA 120
 DB 132 CGATATGTTGCAACTTCTTCCAGGTTAAATGCCAGATAATTCGATACCAAGAA 191
 QY 121 GCGCGGTATCAGATCATCAACGACGAGCTGATGCTTTGACGGGAATCCAGGTTGAATTA 180
 DB 192 GCACATATCAGATCATAAATGATGAACCTGATTTAGATGGAAACCCCAAGGCTGAATTG 251
 QY 181 GCCTCCTTTGTGACGACATGATGGAGCCCTGAGTGTGATAAACTCATCTCTCTCCATC 240
 DB 252 GCTTCTTTTGTATCAACATGATGGAAACCCAGAGTGTGATAAGTTGATGATGACTCTATT 311
 QY 241 AACAGAACTATGTTGACATGAGAGTACCCCGTCAACCGAACTTCAGAACCGATGT 300
 DB 312 AACAGAACTATGTTGATATGATATGATATCTGTTTACCACTGAGCTTCAGATCATGATGT 371
 QY 301 GTGAACATGATGACATCTATTCAATGACACCTGTAGAAGAGCGGAGACCCGCTCGGA 360
 DB 372 GTAAACATGATGATCTCAATTTGTTTATGACCACTTGAAGATGGAGAACTGCGATTGGA 431
 QY 361 GTAGAAACCGTTGGATCATCGAGGCGCATAAATGTTGCCGGTTTGGCCTTCAAGCGTAA 420
 DB 432 GTTGGAACCTGTTGGATCCTCTGAAGCCATTATGCTTGTGATTAGCTTTCAAGAGAAA 491
 QY 421 TGGCAGAACAGCGCAAGCTGAAGCGAACCCTGATAAACCCACACTTGTCAACCGGA 480
 DB 492 TGGCAGAACCAAAATGAAAGCCCAAGGCAACCCCTGTGACAAGCCCAACATTTGACTGT 551
 QY 481 GCCAATGTTCAAGTGTGTTGGGAGAAATTCGCTAGTGTCTTTGAGGTTGAACTTAAAGGAA 540
 DB 552 GCAATGTCCAGGTGTGCTGGGAGAAATTTGCAAGGTATTTTGAAGTGGAGCTTAAAGGAA 611
 QY 541 GTGAATGAGTGAAGGATATGATGAGACCTTCAACAGCTGTTGATATGTTGAT 600
 DB 612 GTAAAGCTTAGTGAAGGATATGATGAGACCTTGAAGAGCTGTGAGATGGTGGAT 671
 QY 601 GAGAACACCATTTGTTGGGACATTTCTTGGTTCCACTCTTAATGGAGAAATTCGAAGAT 660
 DB 672 GAAACACCATTTGTTGAGTGTCTATCTTAGTTTCCACCTCAATGGAGAAATTTGAGAC 731
 QY 661 GTTAAACTTTGAACGATCTCTTGGTCGAAAAAGAACAAAGAAACCGGATGGGATACCA 720
 DB 732 GTTAAAGCGCTGAATGATCTCTTGGTCGAGAGAACAAAGAAACCGGTTGGGACACTCCA 791
 QY 721 ATCCACGTGATGCGGCAAGTGGAGGATTCATTGCAACCGTTTGTGATCGGATTTGGA 780
 DB 792 ATTATGTTGATGAGCAAGTGGTGGATTTATTCACCCGTTCAATACCAGAGCTTGAG 851
 QY 781 TGGGACTTTAGACTTCCCTTGGTGAAGAGATATCAATGTGAGTGTGTCACAAAGTATGACT 840
 DB 852 TGGGACTTTAGATTGCCATTAGTGAAGAGCATTAATGTAAGTGTGTCACAAATATGCTCT 911
 QY 841 GTGTACGAGGATTTGGTGGTGTCTGGAGAAACAAAGAGATTTGCCGTGAGGAACTC 900
 DB 912 GTCTATGCTGTATTTGGTGGTGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 970
 QY 901 ATCTTCCATATCAATATCTTGGTGTGTCGACCAACCCACTTTTACTCTCAATTTCTCCAA 960
 DB 971 ATCTTCCATATTAATTAATCTTGGTGTGTCGATCAACCTTCTCACTCTCACTTTCTTAA 1030
 QY 961 GGTCAAGTCAAGTCATGCTCAATATCACTACCACTTATCCGATGGGCCACGAGGTTAC 1020
 DB 1031 GGTTCAGCCCAAGTAATTTGCTCAATATTACCACTTATTCGCTTGGGTTATGAGGTTAC 1090
 QY 1021 AGAATGTGATGGAGAAATTCAGAGAGAAATATGATCGTCTTAAGGAAAGACTTTGAGAAG 1080
 DB 1091 AAGATGTGATGGAGAAATTTGCAAGAAATATGATCGTCTTATAGAGAGGGCTTAGAAAG 1150
 QY 1081 ACAGAAAGTTCAACATGCTCTCAAGAGAGAGGAGTGCACATTTGCTTTCTCTCTTG 1140
 DB 1151 ACAGAGAGATTCAACATAATCTCCAAAGAAATTTGAGTACCTTTAGTAGCATTTCTCTCT 1210
 QY 1141 AAGATAGCAGCTGTACACTGAGTTCGAATCTCCGACATCTCCGAGTATGATGG 1200

1211 AAAGCAACAGCGAACAACAGAGTTCGAGATTTCTGAAACTTTAAGGAGATTTGGTTGG 1270
 1201 ATAGTGGCGGCTACACATGCTCCAAATGCAACACACATCACTGTTCTTCGTGTGGTT 1260
 1271 ATTGTTCTGTATATACATGCTCCAAAGCGCAACACATTAACAGTTCTCAGAGTTGG 1330
 1261 ATCAGAGAGATTTCTCGAAGCACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
 1331 ATCAGAGAGATTTCTCGGACGTTTGCAGACGACTGGTATAGAGACATCGAAAGTTC 1390
 1321 ATGCGTAGCTGATAGCTTCCTTCGAGAGTATTCACAAAATATCATCTTGGACAGAG 1380
 1391 CTTATGAATTTGACACATCCCTCGACGTTCAATGCTTAAGCTCGTGTGGCCGAGAG 1450
 1381 AAGAGTGAATCTAACAGCGATACTTGTATGTCACGGTGAAGAGCGGATATCGACAAG 1440
 1451 CAGGCGGCTGCAATGGC-----AGCGAGTGCATTAAGAAAACAGATAGCGAGTG 1501
 1441 CAGAGAGATATCATCACTGCTGGAAGAAGTTTGTGCGCCGACAGGAGAAAGACGAGT 1497
 1502 CAGTTGGAGATGATACTGCATGGAAGAAGTTTGTGGAAGAAAAGAAAGAAAGACT 1558

RESULT 5
 AAL43411
 X AAL43411 standard; cDNA; 1665 BP.
 X AAL43411;
 T 25-SEP-2002 (first entry)
 E A thaliana GAD2 coding sequence.
 X GAD; plant GABA production regulation; glutamic acid decarboxylase;
 W plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ss.
 W Arabidopsis thaliana.

X Key Location/Qualifiers
 CDS 17..1501
 T /*tag= a
 T /product= "GAD2"
 X WO200238736-A2.
 N 16-MAY-2002.
 D 07-NOV-2001; 2001WO-US47447.
 F 07-NOV-2000; 2000US-246367P.
 X (EMER-) EMERALD BIOAGRICULTURE CORP.
 X Kinnersley AM, Turano FJ;
 X WPI; 2002-490073/52.
 X P-PSDB; AAO15133.

Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome
 -
 Claim 18; Page 53-54; 63pp; English.
 The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAD), to provide a transformed plant that expresses the GAD coding sequence in response to a signal. Plants of this type have an enhanced

CC ability to tolerate environmental or other stresses. The present sequence
 CC is the A. thaliana GAD2 coding sequence.
 XX
 SQ Sequence 1665 BP; 490 A; 311 C; 423 G; 441 T; 0 other;
 Query Match 57.7%; Score 870.2; DB 24; Length 1665;
 Best Local Similarity 75.1%; Pred. No. 1.7e-256;
 Matches 1110; Conservative 0; Mismatches 348; Indels 21; Gaps 1;
 QY 31 GACGTCCTCCGTCACATCCATCGCATCAGTTCAGTTCGCTACTTCACTTCTAGTTTC 90
 Db 44 GATGAATCTGCTCGACCATGTCGGATCTCGTATGTTTCGCACATCACTTCCCAAGTAT 103
 QY 91 AAGATGCCGGAATACTGATTCCTTAAGGAAGCGCGTATCAGATCATCAACGACGAGCTG 150
 Db 104 GAGATGCTGAGATTCGATACCGAGACGCTGCATATCAGATCATAAAGATGAGCTG 163
 QY 151 ATGCTTGACGGGAATCCACGGTTGAACCTTAGCCCTCTTGTGACGACATGGATGGAGCCT 210
 Db 164 ATGCTTGATGGTAAACCGAGGCTTAACTTAGCTTCTGTTTGTGACTACATGGATGGAACCA 223
 QY 211 GAGTGTGATTAACATCATCTCTCTCCATCAACAAAGAACTATGTTGACATGAGACGAGTAC 270
 Db 224 GAGTGTGACAACTCATCTGACTCTATCAACAGAACTACGTTGATATGATGAGTAC 283
 QY 271 CCCGTACCAACCGAATTCAGAACCGGATGTTGAAACATGATTCACATCTATTCAATGCA 330
 Db 284 CTTGTCAAACTGAGCTCCAGAACCGATGTTAAACATATTAGTCGACTGTTTCAATGCG 343
 QY 331 CCGTTAGAAGAGCGGAGACCGCGTCGAGTAGGAAACCGTTCGATCATCGGAGGCCATA 390
 Db 344 CCATCGAGGAATCTGAGACGCGGTGGGAGTAGGACAGTTGGTCTTCAGAAGCCATC 403
 QY 391 ATGTTGGCGGCTTTGGCTTCAAGCGTAAATGGCAGAAACAGCGCAAGCTGAAGGCATA 450
 Db 404 ATGTTAGCGGATTTGGCTTCAAAAGAAATGGCAGAAACAGCGAGCTGAGGTTAA 463
 QY 451 CCGTTCGATTAACCGAATTCGACCGGAGCCGATGTTCAAGTGTGTTGGGAGAAATTC 510
 Db 464 CTTATGACAAACCCCACTTGTCTAGTGGACCAATGTTCAAGTTTCTGGGAGAAATTC 523
 QY 511 GCTAGTACTTTGAGGTGAACTTAAGGAAGTGAATTTGAGTGAAGGATACTATGTGATG 570
 Db 524 GCTCGTACTTTCGAGGTGGAGCTAAAGGAAGTAAACCTAAGTGAAGTTACTAGTGATG 583
 QY 571 GACCTTCAAGAGCTGTTGATGATGATGAGAACACCAATTTGTTGTTGGGACATCTT 630
 Db 584 GATCCAGACAAAGCAGCAGAAATGTTAGACGAGAAACAATCTGTGTGCGAGCCATAATG 643
 QY 631 GGTTCCTCTTAAATGGAGAAATCGAAGATGTTAAACTCTTGAACGATCTCTTGGTCAA 690
 Db 644 GGATCCACACTCAACGGTGAAGTTCGAAGACGTGAAGCTCTCAATGACTTCTAGTCAAG 703
 QY 691 AAGAACAAAGAAACCGGATGGGATACACCAATCCAGTGGATCGGCAAGTGGAGATTC 750
 Db 704 AAAAAGCAGGAGACTGTTGGAAACACACCCGATCCAGCTGGATGACGCAAGTGGAGGTT 763
 QY 751 ATTGCACCGTTTGTATCCGGATTCGAAATGGGACTTTAGACTTCCCTTGGTGAAGT 810
 Db 764 ATAGTCCGTTTATCTATCTCTGAATTAAGATGGACTTTAGACTTCTTGGTTAAGAGT 823
 QY 811 ATCAATGTGAGTGTCTCAAGTATGGAATGTTGTAACGAGGATTTGGTGGGTGATCTGG 870
 Db 824 ATCAAGCTGAGTGTCTCAAGTATGGAATGTTGTAATGCTGTATGTTGGTGGTGTG 883
 QY 871 AGAAACAAAGAGATTTGCTGAGGAACTCATCTTCCATATCAATTAATCTTGGTGTGAC 930
 Db 884 AGGGCAGCAGAGGATTTGCTGAGAGCTTATCTTTCATATTAATTAATCTTGGTGTGAT 943
 QY 931 CAACCCACTTTTACTCTCAATTTCTCAAAAGGTTCAAGTCAAGTCAATGCTCAATACTAC 990
 Db 944 CAACCCACTTTTCACTCTCAATTTCTCAAGGATTCGAGCCAAATTAATGCTCAATACTAC 1003

781 TGGACCTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGGTCAACAAGTATGGACTT 840
 847 TGGACCTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGGTCAACAAGTATGGACTT 906
 841 GTGTACGACGGATTGGTGGTGAATGTGGAGAAACAAGAGAGATTGGCTGAGGAAGTTC 900
 907 GTCTATGCTGTATGGTGGGCAATTTGGAGGAATAAGGAGACTTGGCTGATGAATTT 966
 901 ATCTTCCATATCAATATCTGGTGGTGAACCAACCCACCTTTACTCTCAATTTCTCCAA 960
 967 ATTTTCCACATCAATATCTGGTGGTGAACCAACCTTTACTCTCAATTTCTCCAA 1026
 961 GGTTCAGAGTCAAGTCAATGTCTCAATATCAATATCAATATCAATATCAATATCAATAT 1020
 1027 GGTTCAGAGTCAAGTCAATGTCTCAATATCAATATCAATATCAATATCAATATCAATAT 1086
 1021 AGAATGTGATGGAGATTTCAGAGAGAAATATGATCGTCTTAAGGAAGAGACTTGAAG 1080
 1087 AAGAATGTGATGGAGATTTCAGAGAGAAATGCAAGGGTATTAAGAGAGAGAAATTTGAAA 1146
 1081 ACAGAAAGGTTCAACATCTCTCAAGACGAGGAGTGCACCTTGTGCTTTCTCTCTTG 1140
 1147 ACTGGAAGATTCAACATCTCTCAAGAGAAATTTGAGTTCCTTAGTATTTCTCTT 1206
 1141 AAGATAGAGCTGTCACTAGTTCGAAATCTCGACATGCTTCGAGGTATGATGG 1200
 1207 AAGACAAACAGTCAACATGATGATGCTGAAATTTCTGAAATCTTGAAGATTTGGATGG 1266
 1201 ATAGTGGCGGCTACAAATGCTCCAAATGCAACACATCACTTCTCTGTTGTT 1260
 1267 ATTGTTCTGGCATTATATGCTCCCAAAATGCTCAACATGTCACAGTTCTCAGAGTTGTC 1326
 1261 ATCAGAGAAGATTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
 1327 ATTAGAGAGATTCTCCGACACTAGCGAGGCGACTGGTAAATAGACATTTGAAAAGTC 1386
 1321 ATGGGTGAGCTCGATGAGTTCCTTCGAGAGTGAATTCACAAAATATATCTTGGACAGAG 1380
 1387 TTCCACGAGTAGACACACTTCCGCGGAGGCTCAACGCTAAGCTAGCCGTGGCGGAGGCG 1446
 1381 AAGAGTGAATCTACAGCGATACTTGTATGTCACGGTGAAGAGAGCGATATCGACAAG 1440
 1447 AATGG-----CAGCGGCGTGCATTAAGAAAACAGATAGAGAGTG 1485
 1441 CAGAGAGATATCATCACTGGCTGGAAGAAGTTTGTCCGACACAGGAGAGAGAGAGT 1497
 1486 CAGCTAGAGATTACTACTGCTGATGTTGAAATTTGTTGCTGATAGAGAGAGAGACT 1542

RESULT 7
 ABZ13132
 ID ABZ13132 standard; DNA; 1482 BP.
 AC ABZ13132;
 QC
 QX
 QY

21-JAN-2003 (first entry)

Arabidopsis thaliana stress regulated gene SEQ ID NO 937.
 Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
 Arabidopsis thaliana.

WO200216555-A2.

28-FEB-2002.

24-AUG-2001; 2001WO-US26685.

24-AUG-2000; 2000US-227866P.

26-JAN-2001; 2001US-264647P.

22-JUN-2001; 2001US-300111P.

XX (Scripps) RES INST.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 XX
 PI Harper JF, Kreps J, Wang X, Zhu T;
 XX
 DR WPI; 2002-304127/34.
 XX
 PT Identifying a stress condition to which a plant cell has been exposed
 and producing plants with increased tolerance to these abiotic stresses
 XX
 PS Claim 144; SEQ ID NO 937; 577pp + Sequence Listing; English.
 XX
 CC The invention relates to identifying a stress condition to which a plant
 cell has been exposed, comprising:
 CC (a) contacting nucleic acid representative of expressed polynucleotides
 in the plant cell with an array or probes representative of the plant
 cell genome; and
 CC (b) detecting a profile of expressed polynucleotides in the plant cell
 characteristic of a stress response. The method is useful in the
 CC production of transgenic plants, cells and seeds and in producing plants
 with increased tolerance to abiotic stress. The present sequence is that
 of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
 in methods of the invention.
 CC Note: The sequence data for this patent is not represented in the printed
 specification but is based on sequence information supplied to Derwent by
 the European Patent Office.
 XX
 SQ Sequence 1482 BP; 402 A; 331 C; 378 G; 371 T; 0 other;

Query Match 56.6%; Score 854.2; DB 24; Length 1482;
 Best Local Similarity 76.0%; Pred. No. 1.3e-251;
 Matches 1054; Conservative 0; Mismatches 333; Indels 0; Gaps 0;
 QY 1 ATGGTCTCTCCCGCGTATCGAGTGGAGTCTCGTCCACTCCATTCGATCA 60
 Db 1 ATGGTCTCTTAAGACAGTTCGAACTGATGCTCAATCCATTCATCTTGTCT 60
 QY 61 CGTTACGTCCTTCTCACTTCTTCCAGTTCGAAAGTCCGAAACTCGATTCCTAAGAA 120
 Db 61 CGTTACGTCCTTCTTCTTCCAGTTCGAAAGTCCGAAACTCAATCCCAAGAA 120
 QY 121 GCGGCTTTCAGATCATCAACGACGAGCTGATGCTTACGCGGAATTCACGTTCAACTTA 180
 Db 121 GCGGCTTTCAGATCATCAACGACGAGCTGATGCTTACGCGGAATTCACGTTCAACTTA 180
 QY 181 GCTCTCTTGTGACGACATGATGAGCTGAGTGTGATAAATCATCATCTCTCCATC 240
 Db 181 GCTCTCTTGTGACGACATGATGAGCTGAGTGTGATAAATCATCATCTCTCCATC 240
 QY 241 AACAGAACTATGTTGATCATGAGCAGATACCCCGTCCACCCGAACTTCAGAACCGATGT 300
 Db 241 AACAGAACTATGTTGATCATGAGCAGATACCCCGTCCACCCGAACTTCAGAACCGATGT 300
 QY 301 GTGACATGATGACATCTTCAATGACCGTTCGAGAGCGGAGAGCGCGTCCGA 360
 Db 301 GTGACATGATGACATCTTCAATGACCGTTCGAGAGCGGAGAGCGCGTCCGA 360
 QY 361 GTAGGAACCGTTCGATCATCGAGGCGCAATATGTTGGCGGTTTGGCTTCAAGCGTAAA 420
 Db 361 GTAGGAACCGTTCGATCATCGAGGCGCAATATGTTGGCGGTTTGGCTTCAAGCGTAAA 420
 QY 421 TGGCAGAACAGCGCAAGCTGAGGCGCAACCGTTCGATTAACCCCAACATGTCACCGGA 480
 Db 421 TGGCAGAACAGCGCAAGCTGAGGCGCAACCGTTCGATTAACCCCAACATGTCACCGGA 480
 QY 481 GCGAATGTCAGTGTGTTGGAGAAATTCGCTAGGTACTTTGAGGTGACTTAAAGGAA 540
 Db 481 GCGAATGTCAGTGTGTTGGAGAAATTCGCTAGGTACTTTGAGGTGACTTAAAGGAA 540
 QY 541 GTGAAATGAGTGAAGGATATCTATGATGGACCCCTCAACAGCTGTTGATGATGTTGAT 600

541 GTGAACCTAAGAGAAGACTATTACGTGATGGACCCCTGTAAAGCGGTCGAAAATGGTAGAC 600
601 GAGAACACCACTTTCTGTTCGGGACATTTCTTGGTTCCACTCTTAATGAGAAATTCGAAGAT 660
601 GAAACACAAATTTGTTCGTGCGTCCATCTCGTTCACGTTAACCGGTGAATTCGAAGAC 660
661 GTTAAACTTTGAACGATCTCTTGGTGGAAAGAACAAAGAAACCGGATGGGATACCA 720
661 GTTAAAGTCTCTCAACGACCTCCTTGTGAGAAAAAACAAGCAACCGGATGGGACGCCA 720
721 ATCCAGCTGGATCGGCAAGTGGAGGATTCATTCACCGCTTTTGTATCCGGATTCGAA 780
721 ATACAGCTGGACGAGCGAGTGGGGTTTATTGCTCCGTTCTTGATCCGAGCTGGAG 780
781 TGGGACTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGGTCAACAGTATGCACTT 840
781 TGGGATTTCCGGCTACCGTTGGTTAAGAGTATTAAATGTGAGTGGTCAACAAATACGGTTG 840
841 GTGTACGAGGATTTGGTTGGTGTATCTGGAGAAAACAAAGAGATTTGCTGAGGAATC 900
841 GTTTACGCGGTATTGGTTGGGTTGTATGGAGAACCAAAACCGATTTGCGCTGATGA 900
901 ATCTTCCATATCAATATCTTGGTGTGACCAACCCACCTTTACTCTCAATTTCTC 960
901 ATCTTCCATATCAATATCTTGGCGCTGATCAACCAACCTTTACACTCAACTTCTC 960
961 GGTTCAGTCAAGTCAATGCTCAATATCACTTATCCGATTTGGGCCACGAGGTTAC 1020
961 GGTTCAGTCAAGTCAATGCTCACTACTACAGCTGATTCGTCTGGATTCGAGGGTTAT 1020
1021 AGAATGTGATGGAGATTCAGAGAGATATGATGCTCTTAAGGAAGGACTTGAAGAG 1080
1021 CGCAATGTGATGGATAATTGTCGGGAAAAATGATGATGATCTAAGACAAGGATTAGA 1080
1081 ACAGAAAGGTTCAACATCGTCTCAAGGAGGAGGTGCCACTTTGTCGCTTTCTCCTTG 1140
1081 ACGGACGTTTAAATCGTCTCCAAAGAAAACGGTGTCCGTTAGTGGCGTTTCTCTC 1140
1141 AAAGATAGCAGCTGTACACTGATGTTGAAATCTCCGACATGCTTGCAGTATGATGG 1200
1141 AAAGATAGTACCGCCCAACAGAGTTCCAGGTGGGCCCATACACTCCGTCGCTTCGG 1200
1201 ATAGTCCGCGCTACACAATGCCCTCCAAATGCCAACACATCACTGTCTTCGTGTT 1260
1201 ATCGTCCGCGCTACAGATGCCCTCCGATGCCGAGCATGTCACITTCCTTCGAGTGT 1260
1261 ATCAGAGAAGATTTCTCCAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAA 1320
1261 ATCCGAGAAGATTTCTCTCGAACCTTAGCCGAGAGATTGGTAGCTGATTCGAGAA 1320
1321 ATGGGTGAGCTCGATGAGCTTCCTTCGAGAGTGATTCACAAATATCACTTGCACAG 1380
1321 CTACAGAGCTCGATAGCTTTCGCGGAGGTTCCGCCAAGATGGCTAATGGAAGA 1380
1381 AAGAGTG 1387
1381 AACGGTG 1387

RESULT 8
AAC36324
ID AAC36324 standard; DNA; 1605 BP.
XX
XX AAC36324;
XX
DT 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 13376.
DE
XX Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX

OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 17-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139482.
PR 18-JUN-1999; 99US-0139484.
PR 18-JUN-1999; 99US-0139485.
PR 18-JUN-1999; 99US-0139486.
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PR 18-JUN-1999; 99US-0139488.
PR 18-JUN-1999; 99US-0139489.
PR 18-JUN-1999; 99US-0139489.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.

30-JUN-1999; 99US-01411287.
 01-JUL-1999; 99US-0141842.
 01-JUL-1999; 99US-0142154.
 02-JUL-1999; 99US-0142055.
 06-JUL-1999; 99US-0142390.
 08-JUL-1999; 99US-0142803.
 09-JUL-1999; 99US-0142920.
 12-JUL-1999; 99US-0142977.
 13-JUL-1999; 99US-0143542.
 14-JUL-1999; 99US-0143624.
 15-JUL-1999; 99US-0144005.
 16-JUL-1999; 99US-0144085.
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 19-JUL-1999; 99US-0144325.
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 19-JUL-1999; 99US-0144333.
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 19-JUL-1999; 99US-0144335.
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 20-JUL-1999; 99US-0144632.
 20-JUL-1999; 99US-0144864.
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 21-JUL-1999; 99US-0145086.
 21-JUL-1999; 99US-0145088.
 22-JUL-1999; 99US-0145085.
 22-JUL-1999; 99US-0145087.
 22-JUL-1999; 99US-0145089.
 22-JUL-1999; 99US-0145192.
 23-JUL-1999; 99US-0145145.
 23-JUL-1999; 99US-0145218.
 23-JUL-1999; 99US-0145224.
 26-JUL-1999; 99US-0145276.
 27-JUL-1999; 99US-0145913.
 27-JUL-1999; 99US-0145918.
 27-JUL-1999; 99US-0145919.
 28-JUL-1999; 99US-0145951.
 02-AUG-1999; 99US-0146386.
 02-AUG-1999; 99US-0146388.
 02-AUG-1999; 99US-0146389.
 03-AUG-1999; 99US-0147038.
 04-AUG-1999; 99US-0147204.
 05-AUG-1999; 99US-0147302.
 05-AUG-1999; 99US-0147182.
 05-AUG-1999; 99US-0147260.
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 06-AUG-1999; 99US-0147416.
 09-AUG-1999; 99US-0147493.
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 10-AUG-1999; 99US-0148171.
 11-AUG-1999; 99US-0148319.
 12-AUG-1999; 99US-0148341.
 13-AUG-1999; 99US-0148565.
 13-AUG-1999; 99US-0148684.
 16-AUG-1999; 99US-0149368.
 17-AUG-1999; 99US-0149175.
 18-AUG-1999; 99US-0149426.
 20-AUG-1999; 99US-0149722.
 20-AUG-1999; 99US-0149723.
 23-AUG-1999; 99US-0149929.
 23-AUG-1999; 99US-0149902.
 23-AUG-1999; 99US-0149930.
 25-AUG-1999; 99US-0150566.
 26-AUG-1999; 99US-0150884.
 27-AUG-1999; 99US-0151065.
 27-AUG-1999; 99US-0151086.
 27-AUG-1999; 99US-0151080.
 30-AUG-1999; 99US-0151303.
 31-AUG-1999; 99US-0151438.
 01-SEP-1999; 99US-0151930.
 01-SEP-1999; 99US-0152363.
 10-SEP-1999; 99US-0153070.
 13-SEP-1999; 99US-0153758.

PR 15-SEP-1999; 99US-0154018.
 PR 16-SEP-1999; 99US-0154039.
 PR 20-SEP-1999; 99US-0154779.
 PR 22-SEP-1999; 99US-0155139.
 PR 23-SEP-1999; 99US-0155486.
 PR 24-SEP-1999; 99US-0155659.
 PR 28-SEP-1999; 99US-0156458.
 PR 29-SEP-1999; 99US-0156596.
 PR 04-OCT-1999; 99US-0157117.
 PR 05-OCT-1999; 99US-0157753.
 PR 06-OCT-1999; 99US-0157865.
 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
 PR 12-OCT-1999; 99US-0158369.
 PR 13-OCT-1999; 99US-0159293.
 PR 13-OCT-1999; 99US-0159294.
 PR 13-OCT-1999; 99US-0159295.
 PR 14-OCT-1999; 99US-0159329.
 PR 14-OCT-1999; 99US-0159330.
 PR 14-OCT-1999; 99US-0159331.
 PR 14-OCT-1999; 99US-0159637.
 PR 14-OCT-1999; 99US-0159638.
 PR 18-OCT-1999; 99US-0159584.
 PR 21-OCT-1999; 99US-0160741.
 PR 21-OCT-1999; 99US-0160767.
 PR 21-OCT-1999; 99US-0160768.
 PR 21-OCT-1999; 99US-0160770.
 PR 21-OCT-1999; 99US-0160814.
 PR 21-OCT-1999; 99US-0160815.
 PR 22-OCT-1999; 99US-0160980.
 PR 22-OCT-1999; 99US-0160981.
 PR 22-OCT-1999; 99US-0160989.
 PR 25-OCT-1999; 99US-0161404.
 PR 25-OCT-1999; 99US-0161405.
 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 51.0%; Score 770; DB 21; Length 1605;
 Best Local Similarity 72.0%; Pred. No. 1e-225;
 Matches 1004; Conservative 0; Mismatches 390; Indels 0; Gaps 0;

QY 17 CCGTATCGGAGTCGGACGTCTCCGTCCACTCCACATTCGCATTCGCTTACGTCGCTACTT 76
 DB 53 CCAACTCTGACTCGACGAGCATTTGCATTCACACTTTTGCCTTCTAGATATGTCGCTGCTG 112
 QY 77 CACTTCTTAGTTCAAGATCGCGAAACTCGATTCCTTAAGGAGCGGCTATCAGATCA 136
 DB 113 TTGTTCCAGGTTCAAGATCGCTGACCATTCGATGCCAAAGATGCTGCTTATCAAGTGA 172
 QY 137 TCAACGACGAGCTGATGCTTGAAGGAACTCCAGGTTGAACCTTAGCTCTTTGTGACCA 196
 DB 173 TCAATGATGATGATGCTTGAAGGAACTCCAGGTTGAACCTTAGCTCTTTGTGACCA 232
 QY 197 CATGGATGGAGCCTGAGTGTGAFAAATCATCATGCTCCATCCATCAAGAACTATGTTG 256
 DB 233 CTTGGATGGAACCTGAGTGTGACAACTCATCATGATTCGTCTCAATAAGAACTATGTTG 292
 QY 257 ACATGAGAGTACCCGCTCACCACGAACTTCAGAACCGATGCTGTAACATGATTCAC 316
 DB 293 ATATGGATGAATATCCTGTCCACATGAGCTCCAGAACCGGTGTGAATATATGATAGCA 352
 QY 317 ATCTATTCAATGACCGTTAGAGAGCGGAGACCGCTCGAGTAGGACCGTTGGAT 376
 DB 353 ACTTTTCCATGCTCCGTTGGAGAGACGAGGCTGCTATTGGGTGGAACTGTTGTTG 412
 QY 377 CATCGAGGCGCAATATGTTGGCGGTTGGCCCTTCAAGCGTAAATGCGAGAACACGCGCA 436

413 CATCTGAGGCTATAATGCTTGTGCTGTTTGGCTTTTCAAAAGGAAATGCGAACATAGGAGAA 472

437 AAGCTGAAGCGAAACCCGTCGATAAACCCAAACATTTGTCACGCGAGCCAAATGTTTCAAGTGT 496

473 AAGCTCAGGCTCTACCTATTGTATAGCCTTAAACATTTGTCACCTGGAGCCAAATGTTTCAAGTGT 532

497 GTTGGGAGAAATTCGCTAGGTACTTTGAGTTTGAACCTTTAAGGAGAGTGAATTTGAGTGTGAAG 556

533 GCTGGGAGAAAGTTTGAAGGTACTTTGAGGTAGAGCTCAAAAGAGGTGAACCTAAGTGAAG 592

557 GATACTATGTGATGGAGCCCTCAACAGCTGTTTGATATGGTTGATGAGAACACCATTTGTG 616

593 ACTACTATGTTATGGATCCAGCTTAAAGCTGTAGAGATGGTGGATGAGAAATACCATCTGTG 652

617 TTGGGAGACATCTTGTTCCACTCTTAATGGAGAGATTCGAGAGATGTTTAAACTCTTGAACG 676

653 TTGAGCGAATTTCTAGAGATCTACCTTACTTGGAGAGTTTGAGAGCTTTAAGCAATTTGAACG 712

677 ATCTCTTTGGTCGAAAAAGAAACAAAGAAACCGGATGGGATACACCAATCCACGTGGATGCGG 736

713 ATCTCTTTAGCTGAGAAAAACCGCAGAGACAGGATGGGAAACTCTTATTCATGTTGATGCGAG 772

737 CAAGTGGAGAGATTCATTTGACACCGTTTCTTCTATCCGGAATTCGGAATGGGACTTTTGAATTC 796

773 CCAGTGGAGAGATTCATTTGCTCTCTTCTCTACCTGATCTTTGAAATGGGACTTTAGGCTTTC 832

797 CCTTTGGTGAAGAGATTCATATGTGAGTGGTTCACAAGTATGGACTTTGTGTACGAGGATG 856

833 CATGGGTGAAGAGATTTAAACGTCAGTGGTTCACAAGTATGGACTTTGTGTATCGAGGAGTTG 892

857 GTTGGGTGATCTCGAGAAACAAAGAGGATTTGCCCTGGAGAACTCATCTTCCATATCAATTT 916

893 GTTGGGTGTCTGGAGAACAAAGATGATTTGCCAGAGAACTTTGTCTTCCATCACTACT 952

917 ATCTTTGGTGTGACCAACCCACTTTACTCTCTCAATTTCTCCAAAGGTTTCAAGTCAAGTCA 976

953 ACTTTGGGAGCTGATCAACCCACTTTCACTCTCAACTTCTCAAAAGGGTTCGAGCCAAATCA 1012

977 TTGCTCTAATCTACCAACTTTATCCGATTCGGATTCGGCCACGAGGTTTACAGAAATGTGATGGAGA 1036

1013 TTGCTCAGTACTACGTTTATCCGACTAGGCTTTTGGGGATACAGAACATATGGAAA 1072

1037 ATTGCAGAGAGATATGATCGTCTTAAAGGGAAGGACTTGAGAGACAGAAAGGTTTCAACA 1096

1073 ACTGCATGGATACCGCAAGGAGCTTAAGAGAGGAATAGAGATGACAGGGAAGTTTCAACA 1132

1097 TCGTCTCAAGAGACGAGGAGTGCCTATGTCGTTCTCTCTTGAAGATAGAGAGCTGTC 1156

1133 TTGTGTCAAAGATATTTGGCGTGCCACTAGTGGCATTTCTCTCAAAGACAGTAGCAAGC 1192

1157 ACATGTAGTTGGAATCTCCGACATGCTTCGCAAGTATGGAATGGAATGTGCGCGCTTACA 1216

1193 ACACGGGTGTTTGATGATCGCAGAGTCTTTGAGAAAAATTCGGGTGGAATCATACCGCTTACA 1252

1217 CAATGCCTCCAAATGACACACATCACTGTTCTTCTGTGTGTTATCAGAGAAATTTCT 1276

1253 CTATGCTGACAGATGCACAGCATTTGCTGCTCAGAGTTGTGATAGAGAGACTTTA 1312

1277 CGAGAACATCTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTGAATGGGTGAGTCTGATG 1336

1313 GCCGAGGCTTTGACAGATGAGACTCATCACACATATCATTTCAAGTGTCTGAAAGAGATTCGAAG 1372

1337 AGCTTCTCTTCGAGAGTGTATTCACAAAATATCACTTGGACAGAGAGAGTGTAACTTCAACA 1396

1373 GGCCTCTCTAGCAGAGTTGCACATCTTGTCTCGCGCTGCACCGGTTAGTGTGATGATGAG 1432

1397 GCGATAACTTGAATG 1410

1433 AAGTTTAAAGTGAAG 1446

ID	AAQ74691	standard; cDNA; 1783 BP.
XX	AAQ74691;	
XX	AAQ74691;	
XX	25-MAR-2003	(updated)
DT	22-JUN-1995	(first entry)
XX		
XX	Early Ripening Tomato protein ERTD1 gene.	
DE		
XX	Early Ripening Tomato; transgenic plant; crop improvement;	
XX	fruit ripening; transformation; ss.	
KW		
XX	Lycopersicon esculentum.	
OS		
XX	WO9421794-A1.	
PN		
XX	29-SEP-1994.	
PD		
XX	22-MAR-1994; 94WO-GB00581.	
XX	22-MAR-1993; 93GB-0005859.	
PR	22-MAR-1993; 93GB-0005860.	
PR	22-MAR-1993; 93GB-0005862.	
PR	22-MAR-1993; 93GB-0005865.	
PR	22-MAR-1993; 93GB-0005866.	
PR	22-MAR-1993; 93GB-0005867.	
PR	22-MAR-1993; 93GB-0005868.	
PR	22-MAR-1993; 93GB-0005869.	
PR	12-JUL-1993; 93GB-0014351.	
PR	12-OCT-1993; 93GB-0020986.	
XX		
XX	(ZONE) ZENECA LTD.	
XX	Abu-Bakar UK, Barton SL, Gallego-Veigas PP, Gray JE;	
PI	Grierson D, Lowe AL, Picton S, Whotton LC, Abubakar UK;	
PI		
XX	WFI; 1994-317014/39.	
DR		
XX	DNA constructs encoding fruit-ripening related proteins - useful	
PT	for transformation of plants to modify fruit quality	
PT		
XX	Claim 1; Page 54; 74pp; English.	
PS		
XX	ERTD1 homologous transcripts are 1.8 kb in size. The transcript	
CC	is found throughout early fruit development of both wild-type and	
CC	rin (ripening inhibitor) fruit. The transcript is detected	
CC	throughout the entire ripening period in rin fruit. The transcript	
CC	is not detected in leaves or wounded leaves of either rin or wild-	
CC	type tomato. The sequence has been deposited as NCIMB 40588. The DNA	
CC	may be used to transform plants for production of plants with an altered	
CC	level of expression. Improvements in transgenic plants include	
CC	resistance to damage and pests, longer shelf life, improved	
CC	flavor/aroma, etc.	
CC	(Updated on 25-MAR-2003 to correct PN field.)	
XX		
XX	Sequence 1783 BP; 512 A; 339 C; 423 G; 509 T; 0 other;	
XX		

	Query Match	48.8%	Score 736.6	DB 15	Length 1783
	Best Local Similarity	71.8%	Pred. No. 2e-215		
	Matches 964	Conservative	0	Mismatches 379	Indels 0
Qy	20	TATCGAGTTCGACGCTCTTCGCTCCACTCCCATTCGCATCCGATCACGTTACGCTCGGTACTCTCAC	79		
Db	28	TAAAGATTCAAGAGAGAGCTTGCACGTGTCACTTTCGATTCAGATATGTACAGGAACCTT	87		
Qy	80	TTCTTAGGTTTCAAAGATGCGGAAAACCTCGATTCTTAGGAAGCGGGGTATCAGATCATCA	139		
Db	88	TACCTAAGTTCAAATGCTTAAATAATCCATGCCGAAGAAGCAGCTTATCAGATTGTAA	147		
Qy	140	ACGACGAGCTGATGCTTCAAGCGGAATCCACGGTTGAACCTTAGTGCTCCTTTGTGACGACAT	199		
Db	148	ACGACGAGCTTATGTTGATGGTGAACCCAGGTTGAAATTTAGCTTCCTTTTAGCACAT	207		

200 GGATGGAGCCTGAGTGTGATAAACTCATCATGTCTCTCCATCAACGAAGAACTATGTGACA 259
|||||
208 GGATGGAGCCGAGTGGGATGAAGTCAATCATGTCTATCCATTATTAAGAACTATGTGACA 267
|||||
260 TGGACGAGTACCCCGTCAACCGAACTTCAGAACCGATGTGTGAACATGATGACATC 319
|||||
268 TGGATGAGTATCTGTGACCACTGAACTTCAAAATAGATGTGTAACTATGTTAGCACATC 327
|||||
320 TATTCAATGACACCGTTAGAGAGCGGAGACCGCGTGGAGTAGGAACCGTTGGATCAT 379
|||||
328 TTTTCCATGCCCCGGTGGTGTGATGAGAGTGCAGTTGGAGTTGGTACAGTGGGTTCAT 387
|||||
380 CGGAGGCCATAATGTTGGCCGGTTCGCTTCAAGCGTAAATGGCGAAGCAAGCGCAAG 439
|||||
388 CAGAGGCAATAATGCTTGTCTGGCTTCTTTTCAAGCGCAATGGCAATCGAAAGAAAG 447
|||||
440 CTGAAGGCAACCGCTCGATTAACCAACCAATGTCTACCGAGCCCAATGTTCAAGTGTGT 499
|||||
448 CAGAGGCAACCGCTTCGATAAGCCTAATATAGTCACTGGAGCTAATGTGCGAGGTCTCT 507
|||||
500 GGGAGAAATTCGCTAGGTACTTTGAGGTTGAACTTAAGGAAGTGAATTTGAGTGAAGAT 559
|||||
508 GGGAAATTTGCAAGGTAATTTGAGGTTGAGTTGAAGGAGGTGAAACTTAAAGAGGAT 567
|||||
560 ACTATGTATGGAGCCCTCAACAGCTGTGATATGTTGATGATGAGAACACCATTTGTGTTG 619
|||||
568 ACTATGTAATGGACCCCTGCCAAGCAGTAGAGATGTGGATGAGATACAATATGTGTTG 627
|||||
620 CGGACATTTCTGTTGTTGCTTCACTTAAATGGAGAAATTCGAAGATGTTAACTCTTGAACGATC 679
|||||
628 CTGCAATCTTGTGTTCTACTCTGACTGGGAGTTTGAGGATGTGAAGTCTCTAAACGAGC 687
|||||
680 TCTTGTGCAAAAGAAACAAAGAAACCGGATGGGATACACCAATCCACGTGGATGCGGCA 739
|||||
688 TCCTTACAAAAGAAACAAAGAAACCGGATGGGAGACACCGATTTATGTCGATGTGCGA 747
|||||
740 GTGGAGATTCATTGACCGCTTTTGTATCCGAATTTGGAATGGGACTTTAGACTTCCT 799
|||||
748 GTGGAGATTTATGCTCTCTCTGTCGACATCTTGAATGGGATTTCCGTTTGCCTTC 807
|||||
800 TGGTGAAGAGTATCAATGTGAGTGGTCAAGATGAGTCTTGTACGAGGAGTGTGTT 859
|||||
808 TTGTGAAAGTATAAATGTGAGCGGTCAAGATGAGTCTTGTATATGCTGTGTCGGT 867
|||||
860 GGGTGTCTGGGAAACAAAGAGATTTGCTGAGGAACTCATCTTCATATCAATATC 919
|||||
868 GGGTGTATGGCGGAGCAAGAGACTTGGCCGATGAACTCGCTTTTCATATAAATCAGC 927
|||||
920 TTGTTGCTGACCAACCCACCTTTTACTCTCAATTTCTCRAAGTTCAAGTCAAGTCA 979
|||||
928 TTGGGTCTGATCAGCTTACTTTTACTCTCAACTTCTTAAAGTTCTTATCAAAATATG 987
|||||
980 CTCAATFACTCAACTTATCGATTTGGGCCACAGGGTACAGAAATGTGATGGAGAAT 1039
|||||
988 CACAGTATTAATCAATTAAGACTTGGCTTTGAGGTTTATAGAACGTCATGAAGAAT 1047
|||||
1040 GCAGAGAGATATCATCGTCTTAAGGAAGGACTTGAAGAGACAGAAAGTTCACATCG 1099
|||||
1048 GCTTATCAACCGCAAAAGTACTACAGAGGAATCAAAAATGCGGGCGGTTCGATTTG 1107
|||||
1100 TCTCAAGGACGAGGAGTGCCACTTCTCGCTTTCTCTCTTGAAGATAGCAGTGTCA 1159
|||||
1108 TCTCTAAGGATGTGGGTGTTCTCTGTGTAGCAATTTTCTCTCAGGGACAGCAGCAATATA 1167
|||||
1160 CTGAGTTGCAATCTCCGACATGTTGCGAGGTATGATGGATGAGTGCAGGCTACAA 1219
|||||
1168 CGGTATTTGAAGTATCTGAGCATCTCAGAGAGATTTGATGGATGATGCGCTGACATACAA 1227
|||||
1220 TGCCTCCAAATGCAACACATCACTGTTCTGCTGTGTTTATCAGAGAGATTTCTCGA 1279
|||||
1228 TGCCACCGGATGCTGAACACATGCTGCTGCTGCGGGTGTCTTATGAGAGGATTTTCAGCC 1287
|||||
1280 GAACACTCGCTGAGAGACTGTGTATGATATAGAGAAAGTGTGCTGAGTCTGATGAGC 1339
|||||

Db 1288 ACAGCCTAGCTGAGAGACTTGTCTTGACATTGAGAAATTTCTGTGAGATTGGACACAC 1347
|||||
Qy 1340 TTCCTTCGAGAGTGTACAAA 1362
|||||
Db 1348 AGCCTCTCTGTTTGGCCACCAA 1370
|||||
RESULT 10
ID AAL43418
ID AAL43418 standard; cDNA; 1783 BP.
XX
AC AAL43418;
XX
DT 25-SEP-2002 (first entry)
XX
Tomato GAD coding sequence.
XX
KW GAD; plant GABA production regulation; glutamic acid decarboxylase;
XX
KW plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ss.
XX
OS Lycopersicon esculentum.
XX
PH Key Location/Qualifiers
XX
FT CDS 6..1514
XX
FT /*tag= a
XX
FT /product= "GAD"
XX
WO200238736-A2.
XX
16-MAY-2002.
XX
07-NOV-2001; 2001WO-US47447.
XX
07-NOV-2000; 2000US-246367P.
XX
(EMER-) EMERALD BIOAGRICULTURE CORP.
XX
Kimmsley AM, Turano FU;
XX
WPI; 2002-490073/52.
XX
P-PSDB; AAO15140.
XX
Making transformed plants that selectively increase gamma-aminobutyric
XX
acid production, by incorporating a DNA construct with a polynucleotide
XX
encoding a plant glutamic acid decarboxylase enzyme into plant's genome
XX
Claim 18; Page 59; 63pp; English.
XX
The present invention relates to a method of producing a transformed
XX
plant that selectively increases production of gamma-aminobutyric acid
XX
(GABA) in response to a signal, by incorporating into the plant's genome
XX
a DNA construct with a non-constitutive promoter operably linked to a
XX
polynucleotide encoding a functional plant glutamic acid decarboxylase
XX
(GAD), to provide a transformed plant that expresses the GAD coding
XX
sequence in response to a signal. Plants of this type have an enhanced
XX
ability to tolerate environmental or other stresses. The present sequence
XX
is the tomato GAD coding sequence.
XX
SQ Sequence 1783 BP; 512 A; 339 C; 423 G; 509 T; 0 other;
Query Match 48.8%; Score 736.6; DB 24; Length 1783;
Best Local Similarity 71.8%; Pred. No. 2e-215;
Matches 964; Conservative 0; Mismatches 379; Indels 0; Gaps 0;
Qy 20 TATCGGAGTGGGAGTCTCGTCCATCCCATTCACATTCGCATCGTTCCTGATTCAC 79
|||||
Db 28 TAAGAGATTTCAGAGAGAGCTTGCCTGTACATTTGCATCAAGATATGTACAGAACTT 87
|||||
Qy 80 TTCCTAGGTTCAAGATGCCGGAACACTCGATTCTTAAGGAAGCGGCTATCAGATCATCA 139
|||||
Db 88 TACCTAAGTTCAAAATGCTTAAATAATTCATGCCGAAGACGCTTATCAGATTGTA 147
|||||

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140 ACACGAGCTGATGCTTTGACGGGAATCCACGGTTGAACCTTAGCCTCTCTTTGTGACGACAT 199
148 ACACGAGCTTATGTTGGATGTTAAACCCAGGTTGAATTTAGCTTCTCTTTGTAGCACAT 207
200 GGATGAGCCTGAGTGTGATAAATCACTCATGATGTCCTCCATCAACAGAACTATGTTGACA 259
208 GGATGAGCCCGAGTGGATAAGCTCATCATGTCATCCATTAATAAAAACTATGTGACA 267
260 TGGACGAGTACCCCGCTCACACCGAACTTCAGAACCGATGTGTGAACATGATTTGCACATC 319
268 TGGATGAGTATCTCTGTCACCACTGAACCTCAAAATAGATGTGTAACAATGTAGCACATC 327
320 TATTCAATGCACCGTTAGAGAGCGGAGACCGCGCTCGAGTAGGAACCGTTGGATCAT 379
328 TTTTCCATGCCCGGTTGGTGATGATGAGACTGCAGTTGGAGTTGGTACAGTGGGTTTAT 387
380 CGGAGGCCATAATGTTGGCGGTTTGGCCCTTCAAGGTAATGGCAGACACAGCGCAAG 439
388 CAGAGGCAATAATGCTTGTGCGCTTGTCTTTCAACGCAAAATGGCAATCGAAAGAAAG 447
440 CTGAAGGCCAAACCGTCGATAAACCACAACTTGTACCGGAGCCAAATGTTCAAGTGTGTT 499
448 CAGAGGCCAAACCTTCGATAAGCCTAATATAGTCACTGAGCTAATGTGCAGGTCGTCT 507
500 GGGAGAAATTCGCTAGATCTTTGAGGTGAACCTTAAAGAAAGTGAATTTGAGTGAAGGAT 559
508 GGGAAAAATTTGCAAGGTAATTTTGAAGTTGAGTTGAAGGAGGTGAAACTTAAAGAGGAT 567
560 ACTATGTGATGGACCTTCAACAGCTGTTGATATGTTGATGAGAACACCATTTGTGTG 619
568 ACTATGTAATGGACCTTCCAAAGCAGTAGAGATAGTGGATGAGAAATCAATATGTGTG 627
620 CGGACATCTTGTGTTCCACTCTTAAATGGAGAATTCGAAGATGTTAAACTCTTTGAACGATC 679
628 CTGAATCTCTGTTTCTACTCTGCTGGGAGTTTGAAGGATGGAAGCTCTTAAACGAGC 687
680 TCTTGTGGAAGAAAGAACAAAGAACCGGATGGGATACACCAATCCACGTGGATCGGCA 739
688 TCTTACAAAAAAGAACAAAGAACCGGATGGGAGACACCGATTCATGTCGATGTGCGA 747
740 GTGAGGATTCATGTGACCGCTTTTGTATCCGGAATTTGGAATGGGACTTTAGACTTCCT 799
748 GTGAGGATTTATGCTTCTCTTCTCTGCGCAGATCTTGAATGGGATTTCCGTTCCCTC 807
800 TGGTGAAGATFATCAATGTGAGTGTGTCACAAAGTATGAGCTTTGTGTACGAGGATTTG 859
808 TTGTGAAAAGTATAAATGTGACGGGTACAAAGTATGGCTTGTATATGCTGTGTCGGT 867
860 GGGTATCTGGAGAAACAAAGAGATTTGCTCGAGGAATCATCTTCCATATCAATATC 919
868 GGGTATGATGGCGGCAAGAGACTTTGCCGATGAACCTCGCTTTTCATATAAATAC 927
920 TTGGTGTGACCAACCCACCTTTTACTCTCAATTTCTCAAGGTTTCAAGTCAAGTCATTG 979
928 TTGGGTCTGATCAGCCTACTTTTACTCTCACTCTCTAAGGTTTCTATCAATATTTG 987
980 CTCATATCTACCAATCTATCCGATTTGGGCCACGAGGTTTACAGAAATGTGATGGAGAAT 1039
988 CACAGTATTATCAGTTAATAAGACTTGGCTTTGAGGCTTATAAGAACGTCATGAAGAAAT 1047
1040 GCAGAGAAATATGATCGTCTTAAGGAAGGACTTTGAGRAGACAGAAAGTTCAACATCG 1099
1048 GCTTATCAACGCAAAAGTACTAAACAGAGGAATTCACAAAAATGGGGCGGTTGATTTG 1107
1100 TCTCAAGGACGAGGAGTGCACCTTGTGCTTTTCTCTTCAAGATAGCAGCTGTGACA 1159
1108 TCTCTAAGGATGTGGTGTCTCTTGTAGCAATTTCTCTCAGGACAGCAGCAATATA 1167
1160 CTGAGTTGCAAAATCTCCGACATGCTTCGAGGATAGATGGAATAGTCCGCGCTTACACA 1219
1168 CGGTATTGTGAAGTATCTGAGCATCTCAGAGATTTGATGGATCGTCCCTGTCATACACA 1227
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QY 1220 TGCCTCCAAATGCACAAACACATCATCTTCTTCTGTTGGTTATCAGAGAAGATTTCTCGA 1279
Db 1228 TGCACCGGATGCTGAACACATTTCTGTACTGCGGTTGTCTATTAGAGAGGATTTTCAGCC 1287
QY 1280 GAACACTCGCTGAGAGACTTGTGATCGATATAGAAAAGTGAATGCGTGAGCTCGATGAGC 1339
Db 1288 ACAGCTAGCTGAGAGACTTGTGATGACATTTGAAAAAATCTGTGAGATTGGACACAC 1347
QY 1340 TTCCTTCGAGAGTGAATTCACAAA 1362
Db 1348 AGCCTCCTCGTTGCCACCAAA 1370

RESULT 11
AAI70004
ID AAI70004 standard; DNA; 1180 BP.
XX AAI70004;
AC AAI70004;
XX
DT 24-JAN-2002 (first entry)
DE Tomato glutamate decarboxylase clone T-gad-19 DNA sequence.
KW Tomato; glutamate decarboxylase; GAD; transgenic plant; T-gad-19; ds.
XX
OS Lycopersicon esculentum.
XX
PN JP2001238555-A.
PD 04-SEP-2001.
XX
PF 13-DEC-2000; 2000JP-0404172.
XX
PR 13-DEC-1999; 99JP-0352552.
PA (AJIN ) AJINOWOTO KK.
XX
WPI; 2001-610050/70.
XX
Creation of a transgenic plant of improved amino acid composition,
involves transformation with antisense sequences -
Example 1; Page 13-14; 18pp; Japanese.
XX
The present invention relates to a method for creating a transgenic plant
which accumulates a larger amount of at least one amino acid of edible
part than a natural plant of the same species cultured under a same
condition. The method involves transforming a plant with a genetic
structure containing an antisense sequence of a gene sequence encoding
glutamate decarboxylase (GAD) and a controlling sequence which can
express the antisense sequence. The resultant transgenic plant has high
added value. The present sequence is the DNA sequence for clone T-gad-19
of the tomato GAD gene, which was used to illustrate the present
invention.
XX
Sequence 1180 BP; 372 A; 188 C; 276 G; 344 T; 0 other;
SQ

Query Match 47.1%; Score 711.4; DB 22; Length 1180;
Best Local Similarity 75.7%; Pred. No. 9.1e-208;
Matches 894; Conservative 0; Mismatches 286; Indels 1; Gaps 1;

QY 112 CCTAAGGAAGCGGCTATCAGATCATCAACGACGAGCTGTGTCAGGGAATCCACGG 171
Db 1 CCAAGGAAGCAGCATATCAGATTTCTTAATGATGAATTAATGTAGATGGAATCCAGG 60
QY 172 TTGAATTTAGCCTCTTTTGTGACGACATGGATGGAGCTGAGTGTGATAAATCATCATG 231
Db 61 TTGAATTTGGCATCTTTTGTGACAACTGATGGAACCCAGAAATGTGACAAATTCATGATG 120
QY 232 TCCTCCATCAACAGAACTATGTTGACATGAGCAGAGTACCCCTCACCACGAACTTCAG 291
Db 121 GATTCCATTAAACAAAATTTATGTTGACATGGATGAATATCTGTCACTGAGCTTCAG 180
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292 AACCGATGTGTGAACATGATTTGCACATCTATTTCATATGCAACCGTTAGAGAGCGCGAGACC 351
181 AATCGGTGTGTAAACATGATAGCGCATTTATTATATGACACCACTTGAAGATGGAGAACT 240
352 GCCGTGGAGTAGGACCGTTGATCATCGGAGGCCATATGTTGGCCGGTTTGCCCTC 411
241 GCAGTTGGAGTTGGAACAGTTGGTTCTTTCAGAGCCATTATGCTTGGATGGCCCTT 300
412 AACGTAATGGCAGAACAGCCAAAGCTGAAGGCAAAACCCGTCATATAAACCCCAACT 471
301 AAGAGAAATGGCAAAACAAATGAAGCCCAAGGAAGCCCTATGATAGCCCAACT 360
472 GTCACCGGAGCCAAATGTTCAAGTGTGTGGGAGAAATTCGTTAGTACTTTGAGGTTGAA 531
361 GTTACTGGTCTAATGTCAGGCTGTGTGGGAAAAATTTGCAAGGTATTTTGAAAGTTGAG 420
532 CTTAAGGAGTGAATTTGAGTGAAGGATATGATGATGACCCCTCAACAAGCTGTTGAT 591
421 CTAAAGAGTGAAGTTGACTGATGATATGATGATGAGCCCTGAGAAAGCTGTGGA 480
592 ATGGTTGATGAGAACACCAATTTGTTGGGCAATTTCTTGGTTCCACTCTTAATGAGAA 651
481 ATGGTTGATGAGAACCAATTTGTTGAGCTGCTATTTTGGTTTCAACTCTGAATGGGAG 540
652 TTCGAGATGTTAACTCTTTGAAGCATCTCTGGTGGAAAGAAACAAAGAACCCGATGG 711
541 TTTGAGGAGTGAAGAAATTTGAATGACCTCTCT-ATTGAAAGAACAAAGGAAACAGGCTG 599
712 GATACACCAATCCAGCTGGATCGGCAAGTGAAGGATTCATTCCACCGTTTGTATCG 771
600 GACACTCAATTCATGTGGATGAGCTAGTGGTGGATTTATTCACACATTTATATCCA 659
772 GAATGGAATGGACCTTGAATTCCTTGGTGAAGAGTATCAATGTAGTGTCAAG 831
660 GAACTTGAATGGACCTTGAATTCCTTGGTGAAGAGTATCAATGTAGTGTCAAG 719
832 TATGAGCTGTGTACGAGGATTTGGTGGTGTATCTGGAGAACAAAGAGATTTGCCT 891
720 TATGGCTTGTATATGCTGTGGTGTGGTGTATATGGCGGAGCAAGGAGACTTGGCC 779
892 GAGGAATCTATCTTCCATATCAATTTGTTGGTGTGACCAACCCACTTTACTCTCAAT 951
780 GATGAATCTATTTTCAATATTAATACCTTGGTGTGATCAACTACTTCACTTCACT 839
952 TTCTCCAAAGGTTCAAGTCAAGTCAATGCTCAATACCACTTATCCGATTTGGCCAC 1011
840 TTCTTAAAGGATCAAGTCAAGTCAATGCTCAATATTTATCAACTAATTCGTTTGGTTAT 899
1012 GAGGTTTACAGAAATGTGTGAGAAATTCGAGAGAAATATGATCGTTCCTAAGGAGGA 1071
900 GAGGTTTATAGAACGTCATGAAGAAATGCTTATCAACGCAAGGGTACTTACAGAGGA 959
1072 CTTGAGAGACAGAAAGGTTCAACATGCTCTCAAGGACGAGGAGTGCCACTTGTGCT 1131
960 ATCAAAAATGGGAAGATTCGAGATTTGCTCCAGGAATGTTGGTGTTCCTTGGTTGCA 1019
1132 TTCTCTTGAAGATGACAGCTGTCACTAGTTTGAATCTCCGACATGCTTCCAGG 1191
1020 TTTTCTCTTAAAGACATAGCAAAACATGATGAGTTTGAAGTCTCTGAAATTTTAAAGGAG 1079
1192 TATGATGATGATGTCGCGCTACACATGCTTCCAAATGCAACACATCACTGTTCTT 1251
1080 TTTGATGATGATGTTCCAGACATACATATGCCACGATGCTTCAACATCACTGATCTT 1139
1252 CGTGTGTTATCAGAGAGATTTCTCGAGAACATCTCGCTGA 1292
1140 AGAGTTGTTATTAGAGAGATTTCTCCCGTACACTGCGCGA 1180

RESULT 12
ID ABX62354
ID ABX62354 standard; DNA; 416 BP.
XX

AC ABX62354;
XX 25-FEB-2003 (first entry)
XX Arabidopsis thaliana expressed sequence related polynucleotide #469.
DE Transgenic plant; plant; genetically modified cell;
XX environmental stress; ribozyme creation; disease resistance;
KW stress tolerance; fungicide screening; insecticide screening;
KW gene; ds.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX US2002040490-A1.
PN 04-APR-2002.
XX 26-JAN-2001; 2001US-0770423.
XX 27-JAN-2000; 2000US-178512P.
PR (GORL/) GORLACH J.
XX (ANY/) AN Y.
PA (HAMI/) HAMILTON C M.
PA (PRIC/) PRICE J L.
PA (RAIN/) RAINES T M.
PA (YUY/) YU Y.
PA (RAME/) RAMEAKA J G.
PA (PAGE/) PAGE A.
PA (MATH/) MATHW A V.
PA (LEDF/) LEDFORD B L.
PA (WOES/) WOESSNER J P.
PA (HAAS/) HAAS W D.
PA (GARC/) GARCIA C A.
PA (KRIC/) KRICKER M.
PA (SLAT/) SLATER T.
PA (DAVI/) DAVIS K R.
PA (ALLE/) ALLEN K.
PA (HOFF/) HOFFMAN N.
PA (HURB/) HURBAN P.
XX Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
PI Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
PI Hurban P;
XX WPI; 2003-110411/10.
XX Novel Arabidopsis thaliana nucleic acid useful for identifying
PT homologous or related genes, and to create genetically modified and
PT transgenic organisms, such as plant cells and plants -
XX Claim 1; SEQ ID NO 469; 43pp; English.
XX The invention describes an Arabidopsis thaliana nucleic acid (I). The
PS polypeptide (II) encoded by (I), transgenic plant (III) or genetically
XX modified cell (IV) are useful for screening a candidate agent for its
CC biological effect, by combining the candidate agent with (II), (III) or
CC (IV), and determining the effect of the candidate agent on (II), (III) or
CC (IV). (I) is useful for identifying homologous or related genes, for
CC producing compositions that modulate the expression or function of its
CC encoded protein, for mapping functional regions of the protein, in
CC diagnosis, for studying associated physiological pathways, for genetic
CC manipulation of cells, preferably plant cells, in screening assays of
CC various plant strains to determine the strains that are capable of
CC withstanding a particular disease or environmental stress, for enhancing
CC or inhibiting production of biosynthetic product in a plant, for
CC producing polypeptides as probes for the detection of mRNA in biological
CC samples, to generate additional copies of (I), to generate ribozymes or
CC oligonucleotides, as single stranded DNA probes or as triple-strand
CC forming oligonucleotides, and to create genetically modified and
CC transgenic organisms, such as plant cells and plants. (II) or (III) is
CC useful for introducing or improving disease resistance and stress

1 tolerance in plants, screening biological active agents, e.g.,
2 fungicides, insecticides, etc., and for elucidating biochemical pathways.
3 (iii) is useful as crops for their enhanced diseased resistance, enhanced
4 traits of interest, for screening programs, as crops which exhibit
5 enhanced tolerance to environmental stress, or to produce a factor. This
6 sequence represents a nucleic acid that may correspond to naturally
7 occurring Arabidopsis thaliana expressed sequences.
8 Note: The sequence data for this patent did not form part of the printed
9 specification, but was obtained in electronic format directly from the
10 US patent office at
11 seqdata.uspto.gov/sequence.html?DocID=99909770423.

2 Sequence 416 BP; 102 A; 114 C; 102 G; 98 T; 0 other;
Query Match 26.6%; Score 402; DB 25; Length 416;
Best Local Similarity 100.0%; Pred. No. 6.7e-113;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
y 1 ATGGTGTCTCCACCGCGTATCGGAGTCGGAGTCCTCGTCCACATCCACATTCGCATCA 60
b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
15 ATGGTGTCTCCACCGCGTATCGGAGTCGGAGTCCTCGTCCACATCCACATTCGCATCA 74
y 61 CGTTAGCTCGTACTTCACCTTCCTAGGTTCAAGATCCGGAACCTCGATTCTTAAGGAA 120
b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
75 CGTTAGCTCGTACTTCACCTTCCTAGGTTCAAGATCCGGAACCTCGATTCTTAAGGAA 134
y 121 GCGGCGGTATCAGATCATCAACGACGAGCTGATCTTGACGGGAATCCACGGTTGAACCTTA 180
b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
135 GCGGCGGTATCAGATCATCAACGACGAGCTGATCTTGACGGGAATCCACGGTTGAACCTTA 194
y 181 GCCTCCTTTGTGACGACATGATGAGGACCTGATGTGATAAATCATCATGTCCTCCATC 240
b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
195 GCCTCCTTTGTGACGACATGATGAGGACCTGATGTGATAAATCATCATGTCCTCCATC 254
y 241 AACAAAGAACTATGTTGACATGGACGAGTACCCCGTCAACACCGAACTTCAGAACCGATGT 300
b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
255 AACAAAGAACTATGTTGACATGGACGAGTACCCCGTCAACACCGAACTTCAGAACCGATGT 314
y 301 GTGAACATGATTGCATCATCTATTCAATGACACCGTTAGAGAGCGGAGACCCCGCTCGGA 360
b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
315 GTGAACATGATTGCATCATCTATTCAATGACACCGTTAGAGAGCGGAGACCCCGCTCGGA 374
y 361 GTAGGACCGTTGGATCATCGGAGGCGCAATATCTTGGCCGGT 402
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375 GTAGGACCGTTGGATCATCGGAGGCGCAATATCTTGGCCGGT 416

RESULT 13

AC44889
D AAC44889 standard; DNA; 1607 BP.
X C
X C
AAC44889;
C C
18-OCT-2000 (first entry)
T T
X X
E Arabidopsis thaliana DNA fragment SEQ ID NO: 44511.
X E
X Arabidopsis thaliana.
W Hybridisation assay; genetic mapping; gene expression control;
W protein identification; signal transduction pathway;
W metabolic pathway; promoter; termination sequence; ss.
X X
X Arabidopsis thaliana.

EP1033405-A2.

PN
XX
06-SEP-2000.
XX
XX
25-FEB-2000; 2000EP-0301439.
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25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.

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PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
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802 TATGACTAGTCTATGCTGTTGTTGGTCTGTGGAGGCGACAGAGGATTTACCT 861
 892 GAGGAATCTCTTCCATATCAATATCTTGGTCTGACCAACCCACCTTTACTCTCAAT 951
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 952 TTCTCCAAAGGTTCAAGTCAAGTCAATCTGCTCAATACCTATCCAACTTATCCGATTGGGCCAC 1011
 922 TTCTCC- AAGGATCGACCAAAATTTATGCTCAATACCTATCCAGCTCAATTCGCTCT----- 974
 1012 GAGGTTACAGAAATGTGATGGAGAATTCAGAG- AGAATATGATGCTCTAAGGGAAG 1070
 975 -----TGAATTCGAGAATTGCATGAAGAACATGTTGTTCTCAAGAAGG 1020
 1071 ACTTGAAGACAGAAAGGTTCAACATCTCTCAAGGACGAGGAGTGCCACTTGTGCG 1130
 1021 TATAGAAACAGAGCGTTCAACATAGTCTCAAGGACCAAGGAGTGCCAGTCTGCTG 1080
 1131 TTTCTCTT- TGAAGAATGAGAGCTGTCACTGAGTTCGAAATCTCCGACATGCTTCGCA 1189
 1081 CTTCTCTCTCAAGGACCATAGTTTCCACACGAGTTCGAGATCTCTGAGATGCTACGTC 1140
 1190 GGTATGATGATAGTCCGCGCTTACCAATGCTCCAAATGCACACATCACTCACTGTTTC 1249
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RESULT 14
 AH23436
 D AH23436 standard; DNA; 1545 BP.
 X AH23436;
 IC
 XT
 Y
 31-JUL-2001 (first entry)
 Aspergillus oryzae glutamate decarboxylase gene related DNA SEQ ID NO: 2.
 Aspergillus oryzae glutamate decarboxylase, gamma-aminobutyric acid enriched food;
 food production; ds.
 Aspergillus oryzae.
 JP2001054390-A.
 27-FEB-2001.
 17-AUG-1999; 99JP-0267604.
 17-AUG-1999; 99JP-0267604.
 (KIKU-) KIKU MASAMUNE SHUZO KK.
 WPI; 2001-276401/29.

XX Glutamate decarboxylase gene for producing protein for use in preparing
 PT gamma-aminobutyric acid enriched food -
 PT
 XX
 PS Disclosure; Page 7; 12pp; Japanese.
 CC The present invention provides a glutamate decarboxylase gene from
 CC Aspergillus oryzae. This can be used to transform an organism which can
 CC then be used in the production of gamma-aminobutyric acid enriched food.
 CC The present sequence is a DNA used in the exemplification of the
 CC invention.
 XX
 SQ Sequence 1545 BP; 373 A; 433 C; 411 G; 328 T; 0 other;
 Query Match 25.6%; Score 386.2; DB 22; Length 1545;
 Best Local Similarity 58.5%; Pred. No. 1e-107;
 Matches 760; Conservative 0; Mismatches 513; Indels 26; Gaps 4;
 QY 52 TTCGATCACTGTTACGTCGCTTCTCACTTCTAGGTTCAAGATGCGGAAAACCTCGATT 111
 DB 112 TACGAAACACGCTTTCGCAACAGAACAGCTGCTCAGACTGAGATGCGGAGCGGAGATG 171
 QY 112 CCTAAGNAGCGGCTATCAGATCATCAACGACGAGCTGATGCTTGACGGAATCCACGG 171
 DB 172 CCCAGAGAGTTCGCTATGCGATGATCAAGACGAGCTGAGCTTCGATGGAACCCCAATG 231
 QY 172 TTGAACCTTAGCTCTCTTTGTGACGACATGATGAGCTGAGTGTGATAAATCATCATG 231
 DB 232 CTCACCTTGGCGAGTTTGTACGACCTATATGGAAGATGAAGCCGAAGAGCTCATGACT 291
 QY 232 TCCTCCATCAACAGAACTATGTTGACATGAGACGAGTACCCCGTCACCCAGAACTTCAG 291
 DB 292 GAATCTCTCAGCAAGAACTTTCATCGATTACGAGGAGTATCCTCAGTCAGCGGAGATCCAG 351
 QY 292 AACCGATGTGTGAACATGATTGACATCTATCAATGCACCGTTTGA- --AGAGCGCGAG 348
 DB 352 AACCGTCTGTCACATGATTGCGCTCTGTTTAAACGCGCAGTTACACGAGAGAGCAG 411
 QY 349 ACCGCGTTCGAGTAGGAACCGTTTGGATCATCGAGGCCATAATGTTGGCGGTTTGGCC 408
 DB 412 CACCGATGGCACCTCGACCATCGATCGTCCGAGCAATCATGCTGGGTACCTCGGCT 471
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 DB 592 GAGGAGCGATATGTGTACTGCACTGAGGACCGCTATGTGATTGATCCCGACGAGCGGTT 651
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 DB 762 --CGATGTTCCCATCCATGTTGACGCGCTAGCGCGGTTTTCGCTGCTCTTCATCAAC 819
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Search completed: October 22, 2003, 11:12:29
Job time : 444 secs

GenCore version 5.1.1.6
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4 protein - protein search, using sw model

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title: US-10-006-852-2

effect score: 2615
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scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 127863 seqs, 47026705 residues

total number of hits satisfying chosen parameters: 127863

minimum DB seq length: 0
maximum DB seq length: 2000000000
Maximum Match 100%
Listing first 45 summaries
Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	2607	99.7	502	1 DCE1_ARATH	Q42521 arabidopsis
2	2250	86.0	500	1 DCE1_PETHY	Q07346 petunia hyb
3	2130	81.5	494	1 DCE3_ARATH	Q42472 arabidopsis
4	2014	77.0	502	1 DCE1_LYCES	P54767 lycopersico
5	1028	39.3	466	1 DCE1_LACIA	Q9CG20 lactococcus
6	1023	39.1	466	1 DCE1_LACIC	Q30418 lactococcus
7	1013	38.7	466	1 DCEA_ECOLI	P80063 escherichia
8	1013	38.7	466	1 DCEB_ECOLI	P28302 escherichia
9	1009	38.6	466	1 DCEA_ECOS7	P58228 escherichia
10	963	36.8	467	1 DCEC_LISIN	Q928k4 listeria in
11	955.5	36.5	462	1 DCEA_LISMO	Q915p3 listeria mo
12	953.5	36.5	467	1 DCEC_LISMO	Q8Y4k4 listeria mo
13	948	36.3	464	1 DCEB_LISIN	Q928r9 listeria in
14	940	35.9	464	1 DCEB_LISMO	Q9eyw9 listeria mo
15	887.5	33.9	585	1 DCE1_YEAST	Q04792 saccharomyc
16	225	8.6	396	1 Y050_METJA	Q60358 methanococ
17	137	5.2	413	1 DCHS_LYCES	P54772 lycopersico
18	127.5	4.9	500	1 DDC_CATRO	P17770 catharanthu
19	124.5	4.8	386	1 DCHS_VTEAN	Q56581 vibrio angu
20	124.5	4.8	510	1 DDC_ACIBA	Q43908 acinetobact
21	123	4.7	480	1 DDC_HUMAN	P20711 homo sapien
22	123	4.7	1935	1 MYH7_HUMAN	P12883 homo sapien
23	123	4.7	1935	1 MYH7_PIG	P79293 sus scrofa
24	121.5	4.6	511	1 DDC_HAEIN	P71362 haemophilus
25	119	4.6	510	1 L2AM_DROME	P18486 drosophila
26	115.5	4.4	656	1 DCHS_RAT	P16453 rattus norv
27	114.5	4.4	756	1 METE_BUCBP	Q89b24 buchnera ap
28	113.5	4.3	804	1 YNAA_CAEEL	P45895 caenorhabdi
29	113	4.3	1934	1 MYH1_MESAU	P13540 mesocricetu
30	112	4.3	593	1 DCP1_PEA	P51850 pisum sativ
31	112	4.3	1935	1 MYH7_RAT	P02564 rattus norv
32	111.5	4.3	377	1 DCHS_KLEPL	P28578 klebsiella
33	110.5	4.2	1420	1 APX_KENLA	Q01613 xenopus lae

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34 109.5 4.2 328 1 L2AM_DROSI
35 108.5 4.1 480 1 DDC_RAT
36 108.5 4.1 625 1 HTPG_BACHD
37 107.5 4.1 377 1 DCHS_MORMO
38 107.5 4.1 662 1 DCHS_HUMAN
39 105.5 4.0 403 1 DDC_DROLE
40 105.5 4.0 536 1 CH60_METAC
41 105 4.0 508 1 DCHS_MANSE
42 104.5 4.0 369 1 DCHS_RHILO
43 104.5 4.0 793 1 YEAB_SCHPO
44 104 4.0 486 1 DDC_PIG
45 104 4.0 847 1 DCHS_DROME

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ALIGNMENTS

```

RESULT 1
DCE1_ARATH
ID DCE1_ARATH STANDARD; PRT; 502 AA.
AC Q42521; Q9FFH9;
DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase 1 (EC 4.1.1.15) (GAD 1).
GN GAD1 OR GDH1 OR GAD OR AT5G17330 OR MKP11.30 OR MKP11_18.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95334488; PubMed=7610159;
RA Azazi T., Baum G., Snedden W.A., Shelp B.J., Fromm H.;
RT "Molecular and biochemical analysis of calmodulin interactions with
RL the calmodulin-binding domain of plant glutamate decarboxylase.";
RL Plant Physiol. 108:551-561(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
RL features of the 1.6 Mb regions covered by twenty physically assigned
RL P1 clones.";
RL DNA Res. 4:215-230(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=97471969; PubMed=9330910;
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RA Shinozaki K., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "RIKEN Arabidopsis full length cDNA clones (RAFLs) sequenced by the
RL SSP consortium (Salk/Stanford/PGEC)";
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS WAY, DIRECTLY
CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
CC BIOSYNTHESIS.
CC -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -!- COFACTOR: Pyridoxal phosphate.
CC -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TRDCL).
CC -----
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CC -----

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R EMBL; U10034; AAA93132.1; -.
R EMBL; AB005238; BAB10520.1; -.
R EMBL; AY094464; AAM19834.1; -.
R InterPro; IPR002129; Pyridoxal dec.
R Pfam; PF00282; Pyridoxal dec; I.
R PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE NEG.
R Lyase; Decarboxylase; Pyridoxal phosphate; Calmodulin-binding;
M Multigene family.
W BINDING 277 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
I T DOMAIN 469 502 CALMODULIN-BINDING.
I T CONFLICT 208 208 A -> D (IN REF. 1).
I T CONFLICT 208 208 A -> D (IN REF. 1).
Q SEQUENCE 502 AA; 57066 MW; 488141FF523E0B22 CRC64;

Query Match 99.7%; Score 2607; DB 1; Length 502;
Best Local Similarity 99.8%; Pred. No. 7.8e-175;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y 1 MVLSHAVSESDVSVHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
b 1 MVLSHAVSESDVSVHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
Y 61 ASFTVTWMEPECDKLIMSSINKNYVDMDEYPTTELQNCVNMIAHLFNAPLEEAETAVG 120
b 61 ASFTVTWMEPECDKLIMSSINKNYVDMDEYPTTELQNCVNMIAHLFNAPLEEAETAVG 120
Y 121 VGTGSSSEAIMLAGLAFKRWQKRAEGKVPDKNIVTGANVQVCWEKFPARYFEVELKE 180
b 121 VGTGSSSEAIMLAGLAFKRWQKRAEGKVPDKNIVTGANVQVCWEKFPARYFEVELKE 180
Y 181 VKLSEGYVYMDPQQAQVDMVDENTICVADILGSTLNGEPEDVKLLNDLLVEKNKETGWDTP 240
b 181 VKLSEGYVYMDPQQAQVDMVDENTICVADILGSTLNGEPEDVKLLNDLLVEKNKETGWDTP 240
Y 241 IHVDAASGFFIAPFLYPELEWDFRLPLVKSINVSGHKYGLVYAGIWMVWRNKEDLPEEL 300
b 241 IHVDAASGFFIAPFLYPELEWDFRLPLVKSINVSGHKYGLVYAGIWMVWRNKEDLPEEL 300
Y 301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQYLIRLGHGEGYRNVMENCRNNMIVLREGLEK 360
b 301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQYLIRLGHGEGYRNVMENCRNNMIVLREGLEK 360
Y 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIVPAYTMPNAQHITVLRVV 420
b 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIVPAYTMPNAQHITVLRVV 420
Y 421 IREDFSRTLAERLVIDIEKVMRELDELPSRVHKSILGQEKSESNDLMVTVKKSIDIK 480
b 421 IREDFSRTLAERLVIDIEKVMRELDELPSRVHKSILGQEKSESNDLMVTVKKSIDIK 480
Y 481 QRDIIITGWKKFVADRKKTSGIC 502
b 481 QRDIIITGWKKFVADRKKTSGIC 502

RESULT 2
CE_PETHY STANDARD; PRT; 500 AA.
D DCE_PETHY Q07346;
C 01-NOV-1995 (Rel. 32, Created)
T 01-NOV-1995 (Rel. 32, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Glutamate decarboxylase (EC 4.1.1.15) (GAD).
N GAD.
DS Petunia hybrida (Petunia).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; famids; Solanales; Solanaceae; Petunia.
DX NCBI_TaxID=4102;
TX [1]
TX SEQUENCE FROM N.A.
TX TISSUE=Petal.
XX MEDLINE=93374956; PubMed=8366104;
XX Baum G.; Chen Y.; Arazi T.; Takatsuji H.; Fromm H.;
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002E2 ARATH STANDARD; PRT; 494 AA.
 003 DCE272;
 004 01-NOV-1997 (Rel. 35, Created)
 005 01-NOV-1997 (Rel. 35, Last sequence update)
 006 28-FEB-2003 (Rel. 41, Last annotation update)
 007 Glutamate decarboxylase 2 (EC 4.1.1.15) (GND 2).
 008 GAD2 OR GDH2 OR AT1G65960 OR F12F19.12.
 009 Arabidopsis thaliana (Mouse-ear cress).
 010 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 011 Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 012 eustosids II; Brassicales; Brassicaceae; Arabidops.
 013 NCBI_taxID=3702;
 014 [1]
 015 SEQUENCE FROM N.A.
 016 STRAIN=cv. Columbia;
 017 MEDLINE=98363649; PubMed=9700069;
 018 "Two isoforms of glutamate decarboxylase in Arabidopsis are regulated
 019 by calcium/calmodulin and differ in organ distribution.";
 020 Plant Mol. Biol. 37:967-975(1998).
 021 [2]
 022 SEQUENCE FROM N.A.
 023 STRAIN=cv. Columbia;
 024 MEDLINE=97267149; PubMed=9112779;
 025 Turano F.J., Thakkar S.S., Fang T., Weisemann J.M.;
 026 "Characterization and expression of NAD(H)-dependent glutamate
 027 dehydrogenase genes in Arabidopsis.";
 028 Plant Physiol. 113:1329-1341(1997).
 029 [3]
 030 SEQUENCE FROM N.A.
 031 STRAIN=cv. Columbia;
 032 MEDLINE=21016719; PubMed=11130712;
 033 Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 034 White O., Alonso J., Altai H., Araujo R., Bowman C.L., Brooks S.Y.,
 035 Bueller E., Chao A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 036 Dunn M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 037 Dunn P., Egtu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 038 Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 039 Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 040 Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kvan A., Lam B.,
 041 Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 042 Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marzilli A.,
 043 Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 044 Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 045 Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 046 Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 047 Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 048 Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 049 "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 050 thaliana.";
 051 Nature 408:816-820(2000).
 052 -!- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
 053 IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
 054 OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
 055 BIOSYNTHESIS (BY SIMILARITY).
 056 -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
 057 -!- COFACTOR: Pyridoxal phosphate.
 058 -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 059 GAD, HDC AND TYRDC).
 060 -----
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 067 or send an email to license@isb-sib.ch.
 068 -----
 069 EMBL; U49937; AAC31617.1; -.
 070 EMBL; U46665; AAC33485.1; -.
 071 EMBL; AC009513; RAF06056.1; -.
 072 FIR; H96683; H96683.

IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
BIOSYNTHESIS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanate + CO(2).
-!- COFACTOR: Pyridoxal phosphate.
-!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).

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EMBL; X80840; CAA56812.1; -;
PIR; S56177;
InterPro; IPR002129; Pyridoxal dec.
Pfam; PF00282; Pyridoxal dec; 1.
PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
W Lyase; Decarboxylase; Pyridoxal phosphate; Calmodulin-binding.
T BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
I DOMAIN 471 502 CALMODULIN-BINDING (BY SIMILARITY).
Q SEQUENCE 502 AA; 56785 MW; 1C5F9BD0084272A6 CRC64;
Query Match 77.0%; Score 2014; DB 1; Length 502;
Best Local Similarity 76.0%; Pred. No. 2.2e-133;
Matches 387; Conservative 53; Mismatches 55; Indels 14; Gaps 5;
1 MVL-SHAVESDVSHSTFASRVVTSLSREKMPENSIPKEAAYQIINDELMDGNPRLN 59
1 MVLTSIRDSSESJCTFASRVVQPLPFKPKMKPKKPAAYQLVDELMDGNPRLN 60
60 LASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTTELQNCVNMIAHLFNAFLAEATAV 119
61 LASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTTELQNCVNMIAHLFNAFLAEATAV 120
120 GVGTVGSSSAIMLAGLAFKRNQKQKAGKPKVDKPNIVTGANVQVCWEKFAFYFEVLK 179
121 GVGTVGSSSAIMLAGLAFKRNQKQKAGKPKVDKPNIVTGANVQVCWEKFAFYFEVLK 180
180 EVKLSEGVYVMDPQOAVDMVDENTICVADILGSLNGEEDVKLLNDLLVEKNKGTGWT 239
181 EVKLSEGVYVMDPAKAVEIVDENTICVAILGSLTGTGEFVKLLNELLTKNKGWET 240
240 PIHVDAAAGGFIAPFLPYBLEWDFRLPLVKSNVSGHKYGLVYAGTGWIMRNKEDLPDE 299
241 PIHVDAAAGGFIAPFLPDLWDFRLPLVKSNVSGHKYGLVYAGTGWIMRNKEDLPDE 300
300 LIPIHNYLGADQPTFLNFSKSSQVIAQYQYQLIRLGHGEGYRNVMENCRNMIVLRGLE 359
301 LVPHINYLGSDQPTFLNFSKSGSYIAQYQYQLIRLGFEGYKNVMKNCLSNKAVLTGKIT 360
360 KTERFNVSKDEGVPLVAPSLKSSCHTTEFSDMLRRYGVIVPVTMPNQAHTVLRV 419
361 KGRFNVSKDGVFPVAPSLRDSKSYTFVSEHLURFEGVIVPVTMPNQAHTVLRV 420
420 VIREDFSRITLABRLVDIKVMRELDELSPSVTHKI - - - - -SLGQKSESNSDNI - - - - -MVTV 473
421 VIREDFSRITLABRLVDIKVMRELDELSPSVTHKI - - - - -SLGQKSESNSDNI - - - - -MVTV 473
474 KXSDIDKQDRIITGWKFFVADRKTTSIGC 502
481 - - - - -ETQKDIHKWRKIAG - - - - -KKTSGVC 502

RESULT 5
CP_LACIA
D DCE_LACIA STANDARD; PRT; 466 AA.
C Q9CG20; O50645;
T T 16-OCT-2001 (Rel. 40, Created)
T T 16-OCT-2001 (Rel. 40, Last sequence update)

DT DE GLUTAMATE DECARBOXYLASE (EC 4.1.1.15) (GAD).
GN GADB OR LIL1290.
OS LACTOCOCCUS LACTIS (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]_TaxID=1360;
RP SEQUENCE FROM N.A., SEQUENCE OF 1-15, AND CHARACTERIZATION.
RC STRAIN=01-7;
RX MEDLINE=99337071; PubMed=10411264;
RA Nomura M., Nakajima I., Fujita Y., Kobayashi M., Kimoto H., Suzuki I.,
ASO H.;
RT "Lactococcus lactis contains only one glutamate decarboxylase gene.";
RL Microbiology 145:1375-1380(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bolotin A., Wincker P., Mauger S., Jaillon O., Malarne K.,
Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
lactis ssp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
CC -!- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES
THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE
(BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanate + CO(2).
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- MISCELLANEOUS: The enzyme is maximally active at pH 4.7. The
activity is stable at acidic pH values; there is no activity in
the neutral pH range. At pH 4.1 the enzyme activity is retained
at temperatures up to 70 degrees Celsius.
CC -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).

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EMBL; AB010789; BAA24585.1; -;
PIR; B86786; B86786.
InterPro; IPR002129; Pyridoxal dec.
Pfam; PF00282; Pyridoxal dec; 1.
PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
W Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 277 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 466 AA; 53926 MW; BCD732253E473C2 CRC64;
Query Match 39.3%; Score 1028; DB 1; Length 466;
Best Local Similarity 45.0%; Pred. No. 1.6e-64;
Matches 195; Conservative 91; Mismatches 141; Indels 6; Gaps 3;
QY 18 FASRYVTSLSRFRKPNPENSIPKEAAYQIINDELMDGNPRLNLAFTVTWMEPCDKLIM 77
DB 18 FGSSEQVDFPKYLAQSQSEPRVAYQLVQDMDLDEGNRLNLATFCQTYMEPEAVKLS 77
QY 78 SSINKNYVDMDEYPTTTELQNCVNMIAHLFNAFLAEATAVGVTVGSSEALMAGLAF 137
DB 78 QTLKNAIDKSEYPRITTEIENRCVNMIAHLFNAFLAEATAVGVTVGSSEALMAGLAF 137
QY 138 KRQWQKKAEGKPDV - - - - -KPNIVTGANVQVCWEKFAFYFEVLKSEGVYVMDPQQA 195
DB 136 KFSWRKRAEKLGLDINAKKPNLVISSSGVQVCWEKFCYWDIEMREVPMDEKHSINDKV 195
QY 196 VDMVDENTICVADILGSLNGEEDVKLLNDLLVEKNKGTGWTPIHVDAAAGGFIAPFL 255
DB 196 MDYVDEYITGVVGINGITTYGRYDDIKALDNLIEYNKQTDYKVIHVDAAAGGFIAPFL 255


```
256 YPELEWDFRLPLVKSINVSHKYLGVYAGIGWVWNRKEDLPBELIFHINYLGAQDPFTT 315
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
256 EPELEWDFSLKNVISINTSGHKYGLVPGVGNVLRDCKKLPBELIFKVSYLGBELPTMA 315
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
316 LNFSGSSQVIAQYQILRLGHEGVNVMNCRENWIVLRBGLKTERFNIVSKDEGVPL 375
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
316 INFHSASQLIGQYVNFYRFGDYKAIHERTHKVMFLAKEIEKTMFENMDGSLQPI 375
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
376 VAFSLKDSCH--TEFEISDMLRRYGVIPAYTPNPAQHITVLRVWIREDFSRTLAERL 433
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
376 VCYKLKEDNSRGNWLYDLADRLLMKGQVPAYPLPKULENEIIQLRIVIRADFGMNAFNY 435
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
434 VIDIEKVMRELDE 446
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
436 VQDMQEAIALNKK 448
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT 6
DE LACLC
D DCE LACLC STANDARD; PRT; 466 AA.
C O30418;
I 16-OCT-2001 (Rel. 40, Created)
I 16-OCT-2001 (Rel. 40, Last sequence update)
I 28-FEB-2003 (Rel. 41, Last annotation update)
E Glutamate decarboxylase (EC 4.1.1.15).
V GAD.
S Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
S Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
X NCBI_TaxID=1359;
X SEQUENCE FROM N.A., AND CHARACTERIZATION.
P STRAIN=MG1363;
X MEDLINE=98143417; PubMed=9404886;
X Sanders J.W., Leenhouts K., Burghoorn J., Brands J.R., Venema G.,
A Kok J.;
T "A chloride-inducible acid resistance mechanism in Lactococcus lactis
T and its regulation.";
L Mol. Microbiol. 27:299-310(1998).
C -!- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES
C THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE.
C -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
C -!- COFACTOR: Pyridoxal phosphate (By similarity).
C -!- INDUCTION: EXPRESSION IS HIGHEST AT ONSET OF STATIONARY PHASE IN
C PRESENCE OF NaCl AND GLUTAMATE, AND AT LOW PH. CHLORIDE-DEPENDENT
C EXPRESSION IS ACTIVATED BY GAD.
C -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
C GAD, HDC AND TYRDC).
C -----
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C or send an email to license@isb-sib.ch).
C -----
C ENBL; AF005098; AAC46188.1; -
C InterPro; IPR002129; Pyridoxal dec.
C Pfam; PF00282; pyridoxal dec; 1.
C PROSITE; PS00392; DDC GAD HDC YDC; FALSE NEG.
C Lysase; Decarboxylase; Pyridoxal phosphate.
T BINDING 277 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
Q SEQUENCE 466 AA; 53849 MW; 28B94EB3FEEB168D CRC64;

Query Match 39.1%; Score 1023; DB 1; Length 466;
Best Local Similarity 45.0%; Pred. No. 3.6e-64;
Matches 195; Conservative 90; Mismatches 142; Indels 6; Gaps 3;

18 FASRYVTSLPFRKMPDNPSTPKAAVQIINDELMDCNPRNLASFVTTWMBPECDKLIM 77
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
18 FGSSEQVDLPKYKLAQQSTPRVAYQLVQDEMDGNAFLNATFCQTYMPEPAVKLMS 77
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
78 SSINKNVDMDEYFVTTQLQNRVCNMIAHLFNAPLEEAETAVGVGTGVSSEATMLAGLAF 137
|||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
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Db 78 QTLKNAIDKSEYPRTEIENRCVNMIADLWNA--SEKGIYGTSTIGSSEACMLGGMAM 135
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 138 KRKQNRKRKAEKGPVD--KPNIVTGANVQVCWEKFARYFEVELKEVKLSEGYVYVMPDQQA 195
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 136 KFSWRKRAEKLGLDINAKKPNLVISISGYQVCWEKFCVYWDIENREVPMDREHMSINLEKV 195
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 196 VDMVDENTI CVADILGSLTNGEPEDVKLNDLLVKKVETGWDTPPIHVDAAAGGFAPFL 255
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 196 MDYVDEYTIQVVGIMGITTYGRYDDIKALDNLNISEYKQTDYKVIYIHVDAASGGLYAPFV 255
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 256 YPELEWDFRLPLVKSINVSHKYLGVYAGIGWVWNRKEDLPBELIFHINYLGAQDPFTT 315
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 256 EPELEWDFRLKNVISINTSGHKYGLVPGVGNVLRDCKKLPBELIFKVSYLGBELPTMA 315
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 316 LNFSGSSQVIAQYQILRLGHEGVNVMNCRENWIVLRBGLKTERFNIVSKDEGVPL 375
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 316 INFHSASQLIGQYVNFYRFGDYKAIHERTHKVMFLAKEIEKTMFENMDGSLQPI 375
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Qy 376 VAFSLKDSCH--TEFEISDMLRRYGVIPAYTPNPAQHITVLRVWIREDFSRTLAERL 433
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 376 VCYKLKEDNSRGNWLYDLADRLLMKGQVPAYPLPKULENEIIQLRIVIRADFGMNAFNY 435
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Qy 434 VIDIEKVMRELDE 446
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db 436 VQDMQEAIALNKK 448
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RESULT 7
DCEA ECOLI
ID DCEA ECOLI STANDARD; PRT; 466 AA.
AC P80063;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN GADA OR GADS OR B3517 OR C4328.
OS Escherichia coli, and
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562, 217992;
RN [1] SEQUENCE FROM N.A.
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=92394884; PubMed=1522060;
RA Smith D.K., Kassam T., Singh B., Elliott J.F.;
RT "Escherichia coli has two homologous glutamate decarboxylase genes
RL that map to distinct loci.";
RN [2] J. Bacteriol. 174:5820-5826(1992).
RN [2] SEQUENCE, AND SEQUENCE OF 148-466 FROM N.A.
RP STRAIN=ATCC 11246;
RC MEDLINE=92155241; PubMed=1740158;
RX Maras B., Sweeney G., Barza D., Bossa F., John R.A.;
RA "The amino acid sequence of glutamate decarboxylase from Escherichia
RT coli. Evolutionary relationship between mammalian and bacterial
RT enzymes.";
RL Eur. J. Biochem. 204:93-98(1992).
RN [3] SEQUENCE FROM N.A.
RP STRAIN=K12 / MG1655;
RX MEDLINE=94316500; PubMed=8041620;
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [4] SEQUENCE FROM N.A.
RP STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX MEDLINE=22388234; PubMed=12471157;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
```

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic *Escherichia coli*."
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

[5] SEQUENCE OF 1-22.
MEDLINE=94033862; PubMed=7764225;
Yoshida T., Yamashino T., Ueguchi C., Mizuno T.;
"Expression of the *Escherichia coli* dimorphic glutamic acid decarboxylases is regulated by the nucleoid protein H-NS";
Biosci. Biotechnol. Biochem. 57:1568-1569(1993).
[6] SEQUENCE OF 382-392.
MEDLINE=97443975; PubMed=9298646;
Link A.J., Robison K., Church G.M.;
"Comparing the predicted and observed properties of proteins encoded in the genome of *Escherichia coli* K-12";
Electrophoresis 18:1259-1313(1997).
-!- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
-!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
-!- COFACTOR: Pyridoxal phosphate.
-!- SUBUNIT: Homohexamer.
-!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC, GAD, HDC AND TYRDC).
-!- DATABASE: NAME=Worthington enzyme manual;
WWW="http://www.worthington-biochem.com/manual/G/GLDP.html".

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EMBL; M84024; AAA33833.1; -;
EMBL; X63123; CAA44834.1; -;
EMBL; U00039; AAB18493.1; -;
EMBL; A5000428; AAC76542.1; -;
EMBL; AE016768; AAN82764.1; ALT_INIT.
PIR; S47737; S24234.
EC02DBASE; D046.5; 6TH EDITION.
EC02DBASE; E046.5; 6TH EDITION.
EcoGene; EG50009; gadA.
InterPro; IPR002129; Pyridoxal dec.
Pfam; PF00282; pyridoxal dec, 1.
PROSITE; PS00392; DDC_GAD_HDC_YDC; 1.
Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family;
Complete proteome.
BINDING 276 276 PYRIDOXAL PHOSPHATE.
CONFLICT 64 64 C -> S (IN REF. 2).
CONFLICT 73 73 H -> R (IN REF. 2).
CONFLICT 153 153 D -> N (IN REF. 2; AA SEQUENCE).
CONFLICT 165 165 C -> S (IN REF. 2).
CONFLICT 208 208 T -> N (IN REF. 2).
CONFLICT 295 295 L -> V (IN REF. 2).
CONFLICT 355 355 D -> N (IN REF. 2; AA SEQUENCE).
SEQUENCE 466 AA; 52685 MW; 86F963E710553E22 CRC64;

Query Match 38.7%; Score 1013; DB 1; Length 466;
Best Local Similarity 45.04; Pred. No. 1.8e-63;
Matches 197; Conservative 83; Mismatches 152; Indels 6; Gaps 3;
16 STFSRVVTSLEPRKPNPENSIPKEAAYQIINDELMDGNPRNLNLASFVTTWPECDKL 75
16 SRFGCAISTIASKPPFLHEMRDDVAFQIINDELMDGNARQNLATFCQTWDDENVHKL 75
76 IMSSINKNYVMDDEYPTVTELOQRNQMIAHLNAPLEAEATVAGTGVGSSEAINLAGL 135
76 MDLSINKNWIDKEEYPSQAIDLCRVNVAIDLHAPAPKNGQAVGNTTIGSSACMLGGM 135

Qy 136 AFKRWKQKKAEGKPVDPKPNVITGANVQVCWEKFPARYEVEVLKVKLSEGYVMDPQQA 195
Db 136 AMKWRKRMEAGKPTDKNLVCGP-VQICMFKFARYWDVLEIRIPMRPGQLFMDPKRM 194
Qy 196 VDMVDENTICVADILGSTLNGEFEDVKLLNDLLVKNKKTGMDTPHVDAAAGGFTAPPL 255
Db 195 IEACDENTIGVFTFGVYTGNYEFPQPLHDAIDKFQADTGIDIDMHIIDAASGGFLAPFV 254
Qy 256 YPELEWDFRLPLVKNSINSGHKYGLVYAGIGVWRNKEDLPEELIFHINYLGAQOPTFT 315
Db 255 APLVWDFRLPRVKSISASGKFLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLGGLG 314
Qy 316 LNFSGKSSQVIAQYQILRLGHEGYRNMCNENMIVLRGLKTERFNIV---SKDEG 372
Db 315 INFSRPAGQVIAQYQYEFRLGREGYTKVQNASYQVAAYLADEIAKLGPEYEFICTGRPDEG 374
Qy 373 VPLVAFSLKDS--CHTEFRISDMLRYGVIIPAYTMPNNAQHITVLRVIREDFSRITLA 430
Db 375 IPAVCFKLKGDGPGYTLDSRLRLRGWQVAFILGGEATDVLVNRIMCRGPFEMDFA 434
Qy 431 ERLVIDIEKVMRELDLP 448
Db 435 ELLEEDYKASIKVLSDEP 452

RESULT 8
ID DCEB_ECOLI STANDARD; PRT; 466 AA.
AC P28302; P76873;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase beta (EC 4.1.1.15) (GAD-beta).
GN GADB OR B1493 OR Z2215 OR ECS2098 OR SF1734.
OS *Escherichia coli*.
OS *Escherichia coli* O157:H7, and
OS *Shigella flexneri*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; *Escherichia*.
OC NCBI_Taxid=562, 83334, 623;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RA MEDLINE=92394884; PubMed=1522060;
RA Smith D.K., Kassam T., Singh B., Elliott J.F.;
RT "Escherichia coli has two homologous glutamate decarboxylase genes that map to distinct loci."
RL J. Bacteriol. 174:5820-5826(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
RT "The complete genome sequence of *Escherichia coli* K-12."
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=E.coli; STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampaio G., Seki Y., Sivasubram S., Tagami H., Takeda J., Takekoshi K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the *Escherichia coli* K-12 genome corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
RN [4]

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SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
[5]
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O157:H7 / RMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
Tada T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
[6]
SEQUENCE OF 1-318 FROM N.A.
SPECIES=E.coli; STRAIN=K12;
Turlin E., Gasser F., Biville F.;
"Sequence and functional analysis of an Escherichia coli DNA fragment
able to complement pqgB and pqgF from Methylobacterium organophilum.";
Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE OF 1-15.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=93204884; PubMed=8455549;
Yoshida T., Ueguchi C., Yamada H., Mizuno T.;
"Function of the Escherichia coli nucleoid protein, H-NS: molecular
analysis of a subset of proteins whose expression is enhanced in a
hns deletion mutant.";
Mol. Gen. Genet. 237:113-122(1993).
[8]
SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
C -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
C -1- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
C -1- COFACTOR: Pyridoxal phosphate.
C -1- SUBUNIT: Homohexamer.
C -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).
-----
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EMBL; M84025; AAA23834.1; --
EMBL; AE000246; AAC74566.1; --
EMBL; D90791; BAA15163.1; --
EMBL; D90790; BAA15157.1; --
EMBL; AE005356; BAB35625.1; --
EMBL; AP002557; BAB35521.1; --
EMBL; X71917; CAA50736.1; ALT SEQ.
EMBL; AE015194; AAN43309.1; ALT_INIT.
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Postfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamouis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
Nature 409:529-533(2001).
[5]
SEQUENCE FROM N.A.
SPECIES=E.coli; STRAIN=O157:H7 / RMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayaishi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Toke T.,
Tada T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli
O157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
[6]
SEQUENCE OF 1-318 FROM N.A.
SPECIES=E.coli; STRAIN=K12;
Turlin E., Gasser F., Biville F.;
"Sequence and functional analysis of an Escherichia coli DNA fragment
able to complement pqgB and pqgF from Methylobacterium organophilum.";
Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE OF 1-15.
SPECIES=E.coli; STRAIN=K12;
MEDLINE=93204884; PubMed=8455549;
Yoshida T., Ueguchi C., Yamada H., Mizuno T.;
"Function of the Escherichia coli nucleoid protein, H-NS: molecular
analysis of a subset of proteins whose expression is enhanced in a
hns deletion mutant.";
Mol. Gen. Genet. 237:113-122(1993).
[8]
SEQUENCE FROM N.A.
SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
MEDLINE=22272406; PubMed=12384590;
Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
Yu J.;
"Genome sequence of Shigella flexneri 2a: insights into pathogenicity
through comparison with genomes of Escherichia coli K12 and O157.";
Nucleic Acids Res. 30:4432-4441(2002).
C -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
C -1- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
C -1- COFACTOR: Pyridoxal phosphate.
C -1- SUBUNIT: Homohexamer.
C -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).
-----
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or send an email to license@isb-sib.ch).
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EMBL; M84025; AAA23834.1; --
EMBL; AE000246; AAC74566.1; --
EMBL; D90791; BAA15163.1; --
EMBL; D90790; BAA15157.1; --
EMBL; AE005356; BAB35625.1; --
EMBL; AP002557; BAB35521.1; --
EMBL; X71917; CAA50736.1; ALT SEQ.
EMBL; AE015194; AAN43309.1; ALT_INIT.
```



```

Rommel B., Rose M., Schluter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294:849-852(2001).
C -1- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
C -1- COFACTOR: Pyridoxal phosphate (By similarity).
C -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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EMBL; AL591983; CAD00512.1; -.
RA PIR; AB1379; AB1379.
RA ListList; LMO02434; -.
RA InterPro; IPR002129; Pyridoxal dec.
RA Pfam; PF00282; pyridoxal dec; 1.
RA PROSITE; PS00392; DDC GAD HDC YDC; FALSE NEG.
W Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
T BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
Q SEQUENCE 467 AA; 53640 MW; 648ACB6FDC82B8CF CRC64;
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Query Match 36.5%; Score 953.5; DB 1; Length 467;
Best Local Similarity 40.4%; Pred. No. 2.6e-59;
Matches 182; Conservative 96; Mismatches 162; Indels 11; Gaps 5;
Y 18 FASRYVTSLSRPFKMPENSIPKEAAQIINDELMDGNPRNLASFTVTWMEPCDKLIM 77
b 19 FGSEESTSPKYLKEPMEPRFAYQLVKDQMDGNARQNLFATFCQTYMEKEAELMA 78
Y 78 SSINKNVVDMDEYPTVELQNCVNIHLNAPLEAEATAVGVGTGSSSEAILAGLAF 137
b 79 ETLEKNAIDKSEYPTAELENRCVNIHLNAPKD--NSYLTGTSTVGSEACMLGLAM 136
Y 138 KRQWQKRAKAGKPV--KPNIVTGANVQVCEKFAFYFEVELKEVLSRGYYVMDPQQA 195
b 137 KFRWRNNAERKGLDIOAKRNLNLISSGYQVCEKFCVYVMDVRVPMKNSLSLDVVKV 196
Y 196 VDMVDENTICVADILGSLTNGEEDVKLLNLLVEKNKEIGWDTPTHVDAASGFIAPFL 255
b 197 FDLVDEYTIQVWGLIGTYTGKFDIQLLDEKVEAYNETNEHQLVHIHDGASGAMTFPFV 256
Y 256 YPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVIRNKSDELPEELIFHINYLGAQDPTFT 315
b 257 NPFLPMDPRLKKNVVSINTSGHKYGLVYPGVWILMKDKYLPKELIFEVSYLGSMPTWA 316
Y 316 LNFSGSSQVIAQYQLIRLHGEGYRNVMNCNRMIVLREGLEKTERFNVSKDGVPL 375
b 317 INFERSASQIGQYFNFLRYGFEGRYIEHKTKTALYLAKTVEKSYFBIINDGANLPI 376
Y 376 VAFSLKDSKC--HTEFEISMLRYGIVPAYTWPNAQHITVLVVIREDFSTLAERL 433
b 377 VCYNKRGELVWETLYDLAQLLWKQGVFAYPELPADLSITIQRFVCRADILGNVAEEF 436
Y 434 VIDIEKVMREIDELPSRVVHKISLGQKSES 464
b 437 AADPADAIHNLH--ARVLYH---DKERNDS 462
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RESULT 13
CEB LISIN STANDARD; PRT; 464 AA.
D DCEB LISIN
C Q928R9;
T 28-FEB-2003 (Rel. 41, Created)
T 28-FEB-2003 (Rel. 41, Last sequence update)
T 28-FEB-2003 (Rel. 41, Last annotation update)
E Glutamate decarboxylase beta (EC 4.1.1.15) (GAD-beta).
N GADB OR LIIN2463.
-----
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
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RC STRAIN-CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Blocher H., Brandt P., Chakraborty T.,
RA Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Fshi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
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RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RA "Comparative genomics of Listeria species.";
RA Science 294:849-852(2001).
CC -1- FUNCTION: Converts internalized glutamate to GABA and increases
CC the internal pH. Involved in glutamate-dependent acid resistance
CC in gastric fluid (By similarity).
CC -1- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TYRDC).
-----
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or send an email to license@isb-sib.ch).
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EMBL; AL596172; CAC97690.1; -.
DR PIR; AB1740; AB1740.
DR ListList; LIN02463; -.
DR InterPro; IPR002129; Pyridoxal dec.
DR Pfam; PF00282; pyridoxal dec; 1.
DR PROSITE; PS00392; DDC GAD HDC YDC; FALSE NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
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Db 194 LDYVDEYTIQVWGLIGTYTGKFDIQLLDEKVEAYNETNEHQLVHIHDGASGAMTFPFV 253
QY 256 YPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVIRNKSDELPEELIFHINYLGAQDPTFT 315
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FT VARIANT 375 375
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FT VARIANT 375 375
FT VARIANT 380 381
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434 VIDIEKVMRELD 445
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28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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GADB OR LMO2363.
Listeria monocytogenes.
Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
NCBI_TaxID=1639;
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STRAIN=LO28 / Serovar 1/2c, and EGD5;
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Cotter P.D., Gahan C.G.M., Hill C.;
"A glutamate decarboxylase system protects Listeria monocytogenes in
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Mol. Microbiol. 40:465-475 (2001).
[2]
SEQUENCE FROM N.A.
STRAIN=EGD-e / Serovar 1/2a;
MEDLINE=21537279; PubMed=11679669;
Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
Charbit A., Chetoui F., Couve E., de Daruvar A., Denoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
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Remmel B., Rose M., Schluter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehlend J., Cossart P.;
"Comparative genomics of Listeria species.";
Science 294:849-852 (2001).
-!- FUNCTION: Converts internalized glutamate to GABA and increases
the internal pH. Involved in glutamate-dependent acid resistance
in gastric fluid.
-!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
-!- COFACTOR: Pyridoxal phosphate (By similarity).
-!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).
-----
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or send an email to license@isb-sib.ch).
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EMBL; AF309077; AAC22562.1; -.
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Pfam; PF00282; pyridoxal dec; 1.
PROSITE; PS00392; DDC GAD HDC YDC; FALSE_NEG.
Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
BINDING 275 275 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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FT VARIANT 92 92
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FT VARIANT 375 375
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Query Match 35.9%; Score 940; DB 1; Length 464;
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Matches 179; Conservative 93; Mismatches 154; Indels 6; Gaps 3;

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Db 76 ETELEKNAIDKSEYPTAELENRCVNIADLWHAPKD--QKFMGTSTIGSSEACVLGGMAM 133
QY 138 KRKQNKRAEGKPV--DKPNIVTGANVQVCKEPARYFEVELKEVKLSBGYYVMDPQQA 195
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QY 196 VDMYDENTICVADILGSTLNGEPEDVKLLNDLVEKNKETGWDTPIHVDAASGGFIAPFL 255
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DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
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RC STRAIN=S288c / AB972;
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RA Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S.,
RA Jagels K., Lye G., Moule S., Odell C., Pearson D., Rajadream M.A.,
RA Rice P., Skelton J., Walsh S., Whitehead S., Bartell B.G.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome
RT XIII.";
RL Nature 387:90-93 (1997).
CC -!- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -!- COFACTOR: Pyridoxal phosphate (By similarity).
CC -!- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
GAD, HDC AND TYRDC).
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

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Listing first 45 summaries

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AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
 Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of
 Overgo Probes
JOURNAL Unpublished (2002)
REFERENCE 2 (bases 1 to 1168)
AUTHORS Coe,E.H.
JOURNAL Direct Submission
TITLE Submitted (25-APR-2002) Maize Mapping Project, University of
 Missouri, Columbia, MO 65211, USA
COMMENT If you are interested in getting corresponding physical clones,
 these are publicly available from ZmDB and may be found by BLAST
 searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; RIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.
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 VERSION CB655721.1
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 ORGANISM Oryza sativa (japonica cultivar-group)
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 Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
 Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
 Large-scale identification of ESTs involved in the interaction
 between rice and Magnaporthe grisea
 Unpublished
 Contact: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
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 BACKWARD: gga aac agc tat gac cat g

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        363 GTGAAGCTGAGTGCAGCTACTAGTCAATGAGCCAGCTAAGCCGCTGATATGTCGAC 422
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        423 GAGAACCACTCTCGCTCGCGCGATCTCGGTCGACGCTGAACGGGGAGTTTCGAGGAC 482
        221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240
        483 GTGAAGCTGCTCAACGATCTCTCACCAGAAGAAACCGCTGAACAGGCTGGACACGCCG 542
        241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
        543 ATCCAGCTGGACGGCGAGCGGGGTTCATCGCGCGTTCCTGTACCGGAGCTGGAG 602
        261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
        603 TGGGACTTCCGCTGCCGCTGCTGAAGAGCATCAACGTGAGCGGGCACAAGTAGCGGCTC 662
        281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300
    Db
        663 GTCTACGCCGGATCGGTGTGTCATCTGGAGGACGAAGGAGGATCTCGCTGAGGAGCTC 722
    QY
        301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
    Db
        723 ATCTTCCACATCACTACTCTGCGCGCGACGACGACCTTCACCTCACTTCTCCAG 782
    QY
        321 GlySerSerGlnValIleAlaGlnTyr 329
    Db
        783 GGGTTTCAGCCAGGTTCATTCACAGTAT 809
    RESULT 3
    BE040860
    LOCUS
    DEFINITION
        BE040860 OF Oryza sativa cdna 5' similar to glutamate decarboxylase
        1, mRNA sequence.
    ACCESSION
        BE040860
    VERSION
        BE040860.1
    GI:8336367
    KEYWORDS
        EST.
    SOURCE
        Oryza sativa
    ORGANISM
        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
        Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
        Ehrhartoideae; Oryzeae; Oryza.
    REFERENCE
        1 (bases 1 to 821)
    AUTHORS
        Bohnert,H.J.; Borchert,C., Brazille,S., Brooks,J., Baton,M., Ferrea
        H., Kawasaki,S., McColough,A., Michalowski,C.B., Palacio,C.,
        Scara,G., Wheeler,M. and Zepeda,G.R.
    TITLE
        Functional Genomics of Plant Stress Tolerance
    JOURNAL
        Unpublished
    COMMENT
        Contact: Michalowski,C.B.
        University of Arizona
        Bio Sciences West room 513, Tucson, AZ 85721, USA
        Tel: 520-621-7982
        Fax: 520-621-1697
        Email: cbm@u.arizona.edu
        An open reading frame exists.
        Insert length: 1 Std Error: 0.00.
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                /clone_lib="Op"
                /note="1 week 150mM NaCl"
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    Alignment Scores:
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        Score:          1281.00         Matches:      243
        Percent Similarity: 94.42%      Conservative: 11
        Best Local Similarity: 90.33%      Mismatches:  15
        Query Match:      48.99%         Indels:       1
        DB:              10            Gaps:        0
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        46 IleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeuAlaSerPheValThr 65
    Db
        9 ATCAACGACGAGCTGATGTGACGCGCAACCGCGGCTGAACCTCGCTCGTTCGTACC 68
    QY
        66 ThrTrpMetGluProGluCysAspLysLeuIleMetSerIleAsnLysAsnTyrVal 85
    Db
        69 AGTGTGATGGAGCCCGAGTGGACAGCTCATCCAGGCTTCGTCGATGATGATGATGCA 128
    QY
        86 AspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCysValAsnMetIleAla 105
    Db
        129 GACATGGACGAGTACCCCGCTCACCCGAGCTCCAGAACCGATGTGTGACATGATGCA 188
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106 HisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGlyValGlyThrValGly 125
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126 SerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLysTrpGlnAsnLysArg 145
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249 TCCTCTGAGGCCATCATGCTCGCGGTTTGCCCTTCAAGAGGAGTGGCAGAACAGATG 308
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146 LysAlaGluGlyLysProValAspLysProAsnIleValThrGlyAlaAsnValGlnVal 165
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309 AAGCAGCCGCAAGCCATCGACAGCCCTAACATTGTCACCGCGCCCAATGTCGAAGTT 368
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166 CysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGluValLysLeuSerGlu 185
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369 TGTGGGAGAAGTTCGCGCATACTTCGAGGTTGAGCTCAAGGAAGTGAAGCTGAGTGAC 428
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186 GlyTyrTrpValMetAspProGlnGlnAlaValAspMetValAspGluAsnThrIleCys 205
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429 GGTACTACGTCTATGGACCCAGCTAGCGCGTGGATATGTCGACGAGAACACCATCTGC 488
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206 ValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAspValLysLeuLeuAsn 225
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489 GTCGCGCGCATCTCGGTCGACGCTGAACGGGAGTTTCGAGGACGTGAAGCTGCTCAAC 548
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226 AspLeuLeuValGluLysAsnLysGluThrGlyTrpAspThrProIleHisValAspAla 245
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549 GATCTGCTCCACGAAGAAGACGCTGAACAGAGTGGGACACGCGCATCCAGTGGACGG 608
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246 AlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGluTrpAspPheArgLeu 265
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266 ProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeuValTyrAlaGlyIle 285
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669 CCGCTGTGTGAAGAGCATCAAGTGGAGGGCCACAGTACGGGCTCGTCTACGCGGGATT 728
|||||
286 GlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeuIlePheHisIleAsn 305
|||||
729 CGGTGGTGCATCTGGGAGACGAAGGAGATCTGCTGAGGAGCTCATCTTTCACATAACT 788
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306 TyrLeuGlyAlaAspGlnProThrPhe 314
|||||
789 TACT--GGNGCCGACAGGCCACTTTTAC 813
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RESULT 4
F275438
OCUS
EFINITION
arborescens cDNA clone GA_Eb0024A19f, mRNA sequence.
ACCESSION
F275438
VERSION
F275438.1
KEYWORDS
GI:11206508
SOURCE
Gossypium arboreum
ORGANISM
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 837)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL
Unpublished
COMMENT
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCATATAGGG
High quality sequence start: 2
High quality sequence stop: 718.
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/organism="Gossypium arboreum"
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/db_xref="taxon:29729"
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/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT      244 a 171 c 198 g 223 t
ORIGIN

Alignment Scores:
Pred. No.:      3,98e-138      Length:      837
Score:          1279.00      Matches:    248
Percent Similarity: 94.80%      Conservative: 7
Best Local Similarity: 92.19%      Mismatches: 14
Query Match:      48.91%      Indels:      1
DB:               10          Gaps:         0

US-10-006-852-2 (1-502) x BF275438 (1-837)
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QY      21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
DB      92 CGTTATGTCGGAACCTCACTGCCAGGTTCAAAATGCCAGAAACTCCATACCAAAAGAG 151
QY      41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
DB      152 GGTGTTATCAGATCATCAATGATGACTGATGCTTGTATGGCAACCCCAAGTTGAACCTT 211
QY      61 AlaSerPheValThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
DB      212 GCCTCTTTTGTACTACATGGATGGAGCTGAATCTGATAGCTTATAATGGACTCCATC 271
QY      81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
DB      272 AACAAAGAACTACGTTGACATGATGAATACCCCTGTCAACACTCAGCTTCAGAAATCGTTGT 331
QY      101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
DB      332 GTGAACATGATAGCACATCTTTTCAACGCACCATTTGGGAGAGTCAGAGGCAGCAGTTGGT 391
QY      121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
DB      392 GTGGGAACAGTTGGGTTCATCGGAGGCAATCATGTTGGCTGGCTTGTCTTCAAGAGAAAA 451
QY      141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
DB      452 TGCAGAAAACAAACGTAAGGCTCAAGGCAACCTTATGAAAGCCGAAATATCGTGAATGGA 511
QY      161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
DB      512 GCCAATGTCAGGTTGCTGGGAGAAATTTGCAAGGTACTTTGAAGTGGAGTTGAAGAA 571
QY      181 ValLysLeuSerGluGlyTyrTrpValMetAspProGlnGlnAlaValAspMetValAsp 200
DB      572 GTGAAGCTTAGAGAAGGGTACTATGTGATGGACCTGTCAAGCAGTGGAAATGTTGAT 631
QY      201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
DB      632 GAAACACCATCTGTGTAGCTCAATCTTGGGTTTCAACCCCTCAATGGAGAAATTTGAAAGAT 691
QY      221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrProAspThrPro 240
DB      692 GTCAAGCTTCTAAACGATCTTTTAATTTGAAGAGACANA-GAAACTGGATGGATACCCCC 750
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	261	TTrpAspPheArgLeuProLeuValLys	269
	811	TGGGACTTCGAAGGCTCCCCCTGTGAAG	837
RESULT 5	BQ165651	819 bp mRNA linear EST 25-APR-2002	
LOCUS	EST611520	KVXC Medicago truncatula cDNA clone pKVXC-10G4, mRNA	
DEFINITION	sequence.		
ACCESSION	BQ165651		
VERSION	BQ165651.1	GI:20308272	
KEYWORDS	EST.		
SOURCE	Medicago truncatula (barrel medic)		
ORGANISM	Medicago truncatula		
REFERENCE	1 (bases 1 to 819)		
AUTHORS	VandenBosch,K., Endre,G., Silverstein,K, Town,C.D., Van Aken,S., Utterback,F., Cheung,F. and Fraser,C.M.		
TITLE	The Medicago truncatula 'kiloclone' set; ESTs selected and re-arrayed from various libraries		
JOURNAL	Unpublished		
COMMENT	Contact: VandenBosch K Department of Plant Biology University of Minnesota 220 Biosci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA Tel: 612 624 2755 Fax: 612 625 1738 Email: kvandenb@chs.umn.edu TIGR sequence name: MTNAJ76TK Alias Clone name:MHAM-5712 More information is available at: www.medicago.org Seq primer: SKmod (CTA gAA CTA gTG GAR CC).		
FEATURES	Location/Qualifiers		
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	/lab_host="XL0LR"		
	/clone_lib="KVXC"		
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BASE COUNT	245 a 158 c 188 g 228 t		
ORIGIN			
Alignment Scores:			
red. No.:	1..13e-137	Length:	819
core:	1275.00	Matches:	245
Percent Similarity:	95.44%	Conservative:	6
Best Local Similarity:	93.16%	Mismatches:	11
Query Match:	48.76%	Indels:	1
Gaps:	13	Gaps:	0
S-S-10-006-852-2 (1-502) x BQ165651 (1-819)			
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	32	GTTCCTCAAGACAGCCTCGAGTCTGATGCTGTGCTCATCAACCTTGTCTGC	91

JOURNAL
COMMENT

http://comgenomics.ucdavis.edu/
 Unpublished
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozik@ucdavis.edu [michelmoreveg@mail.ucdavis.edu]
 belongs to contig QH_CA_Contig2686, see http://cgdb.ucdavis.edu/
 for details
 Plate: QHG17 row: F column: 24.

FEATURES
source

Location/Qualifiers
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 TAG_LIB=QH_EFGHJ sunflower RHA280
 TAG_TISSUE=huills
 TAG_SEQ=GCTAGTCGGG"

ASE COUNT 224 a 140 c 191 g 219 t 1 others

RIGIN

Ligment Scores:

red. No.: 6.96e-132 Length: 775
 core: 1225.00 Matches: 228
 percent Similarity: 94.57% Conservative: 16
 est Local Similarity: 88.37% Mismatches: 14
 very Match: 46.85% Indels: 0
 B: 13 Gaps: 0

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 141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
 61 TGGCAAAACAAAATGAAAGCTCTTGGCAACCTTGGCAACCTTAACTTGAACCGGG 120
 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
 121 GCCAACCTTCAGGTTTGTGGAGAAATTTGCTCGGTATTTTGAAGTGGAGTTGAAGAA 180
 181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
 181 GTGAAGTTGAGGAAGGTACTACGTGATGATCTGAGAAAGCTGTGGAGATGGTTGAT 240
 201 GluAsnThrIleCysValAlaAspIleIeuGlySerThrLeuAsnGlyGluPheGluAsp 220
 241 GAAACACACTATTTGTGTGGCTGCTATCTTGGTTCACCTCACTCAATTTGAAGAT 300
 221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240
 301 GTTAAGCGTTTAAATGACCTCTTGAATGAGAAATGCCAAGACCGGATGGGATACACCT 360
 241 IleHisValAspAlaAsnGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
 361 ATTCATGTGGACGTCGACAGTGGAGGTTTATTGCACCATTTATTATCCCGGAACTTGAA 420

QY 261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
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 QY 281 ValTyrAlaGlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300
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 QY 301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
 DB 541 ATCTTTACATCAACTATCTTGGTGGTGAACCACTTTCATCTCAACTTCCTCCAAA 600
 QY 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
 DB 601 GGTTCAGTCAATAATTTGCTCAATCTATCAGTTCATTCGTTGGTTCGAGGGATAC 660
 QY 341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlyLys 360
 DB 661 AAGAGTATCATGGAATACTGTNCAGAAATGCAAAATGTTCTAAAGAAAGGTTTGGAGAA 720
 QY 361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPhe 378
 DB 721 ACCGACGGTTCAACATCATCTCTAAGAACACGCGCTCCCACTTGTAGCTTC 774

CAB13481 786 bp mRNA linear EST 11-APR-2003
 CA48LN10IF-E8 Cabernet Sauvignon Leaf - CA48LN Vitis vinifera cDNA
 clone CA48LN10IF-E8 5', mRNA sequence.
 CAB13481
 VERSION CAB13481.1 GI:26262418
 KEYWORDS EST.
 SOURCE Vitis vinifera
 ORGANISM Vitis vinifera
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
 ; Vitaceae; Vitis.
 1 (bases 1 to 786)
 ,M.A. and Cook,D.R.
 Transcriptional responses of Vitis vinifera to infection by the
 bacterial pathogen Xylella fastidiosa
 Unpublished
 Contact: Doug Cook
 CAES Genome Facility
 UC Davis Department of Plant Pathology
 1 Shields Ave., Davis, CA 95616, USA
 Tel: 530 754 6561
 Fax: 530 754 6617
 Email: drcook@ucdavis.edu
 Seq primer: GTTATCAGTCGACGGTACC.
 Location/Qualifiers
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 /lab_host="DH5alpha"
 /clone_lib="Cabernet Sauvignon Leaf - CA48LN"
 /note="Organ: Leaf; Vector: pDNR; Site: 1: Sfil; Site 2:
 Sfil; CA48LN is a cDNA library of Cabernet Sauvignon
 leaves. The leaves were collected on September 20, 2001,
 in Napa Valley, California, and represent leaves in late
 season development. These leaves were asymptomatic and
 verified to be non-infected with the bacterial pathogen,
 Xylella fastidiosa, based on a diagnostic assay using PCR
 and Xylella-specific primer pairs. cDNAs were made by
 oligo-dT priming and directionally cloned. 5' and 3'
 adaptors were used in cloning as follows:

FEATURES
source

5'-AAGAGTGGTATCAACGACGAGTGGCCATTACGGCGGG-3' and
5'-ATTCTAGAGCCGAGCGGCACATG-GT(30)NN-3'. Library was
constructed using the Clontech Creator SMART kit and
size-selected to contain the 0.5-3 kb size fraction."

ASE COUNT 222 a 163 c 200 g 201 t
RIGIN

lignment Scores:

red. No.: 2,72e-131 Length: 786
core: 1220.00 Matches: 232
percent Similarity: 95.42% Conservative: 18
est Local Similarity: 88.55% Mismatches: 12
uery Match: 46.65% Indels: 1
B: 14 Gaps: 0

S-10-006-852-2 (1-502) x CA813481 (1-786)

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b 61 GCAGTGGAGATGGTGGACGAGAACACCATCTGTGTGCTGCTATCCTTGGTCTACCCCTC 120
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215 AsnGlyGluPheGluAspValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGlu 234
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b 121 AATGGAGAATTCGAAGATGTTAAACACTTCAATGATCTTTTGACAAAGAAAACAAAGAA 180
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355 ArgGluGlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGlyValPro 374
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b 661 CTGGAGCTATGATGATGTCGTCAGCTTATACCATACCGCGGATGCACAACTGTG 720
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415 ThrValLeuArgValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuVal 434
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b 721 ACTGTTCTTCTGTCGTCATPAGAGAGA-TTCTCGGGCACACTTGTCTGAGCGCTTGGTC 779
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435 IleAsp 436
780 ACAGAT 785
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RESULT 8
BF263784
LOCUS
DEFINITION

BF263784 823 bp mRNA linear EST 23-OCT-2001
HV_CEA0007K14f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Blumeria challenged) Hordeum vulgare subsp. vulgare
cDNA clone HV_CEA0007K14f, mRNA sequence.

BF263784
BF263784.2 GI:13261070

EST.
Hordeum vulgare subsp. vulgare

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.

1 (bases 1 to 823)

Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
for barley genomics: Blumeria infected incompatible (Mla13)

seedling leaf cDNA library

Unpublished

On Nov 17, 2000 this sequence version replaced gi:11194778.

Contact: Wing RA

Clemson University Genomics Institute

Clemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 4293

Email: rwing@clemson.edu

Total hq bases = 571

Seq primer: AATTAACTCTCACTAAAGGG

High quality sequence stop: 721.

Location/Qualifiers

FEATURES
source

1..823

/organism="Hordeum vulgare subsp. vulgare"

/mol_type="mRNA"

/cuiTovar="CI16155 (Mla13)"

/db_xref="taxon:112509"

/clones="HV_CEA0007K14f"

/tissue_type="seedling green leaf"

/lab_host="TJCI21"

/clone_lib="Hordeum vulgare seedling green leaf EST

library HVCDNA0004 (Blumeria challenged)"

/note=vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;

C.I. 16155 (Mla13) plants were greenhouse grown in the R
Wise lab at Iowa State University, Ames, IA; 7 day old

green seedlings were challenged with isolate A27 (AvrMla13
) of Blumeria graminis f. sp. hordei and leaves were

harvested 20 and 24 hr post-inoculation and snap frozen;

uninoculated leaves were harvested 20 hr post-inoculation

(Wei, Wise). In the TJ Close lab at the University of

California, Riverside, total RNA was prepared from each

sample pool, equal quantities of all three RNA pools were

combined, poly(A) RNA was purified from the mixture, one

cDNA library was made, and 1 million pfu were in vivo

excised to give pBluescript SK(-) cDNA phagemids (Choi,

Close). Phagemids were plated and picked at the Clemson

University Genomics Institute (CUGI) (Begum, Palmer,

Frisch, Atkins and Wing). Plasmid DNA preparations, DNA

sequencing and sequence analysis were performed at CUGI

(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).

The sequence has been trimmed to remove vector sequence

and contains a minimum of 100 bases of phred value 20 or

above. For more details on library preparation and

sequence analysis see

http://www.genome.clemson.edu/projects/barley. To order

this clone see http://www.genome.clemson.edu/orders Also

see Close TJ, Wing R, Kleinhofs A, Wise R (2001)

Genetically and physically anchored EST resources for

barley genomics. Barley Genetics Newsletter 31:29-30.

(http://wheat.pw.usda.gov/ggpages/bgm/31/cover.html)"

a 187 c 249 g 175 t 3 others

BASE COUNT


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181 ValLysLeuSerGluGlyTyrValMetAspProGlnAlaValAspMetValAsp 200
181 GTGAAGTTGAGGAAGCTTACTACGTGATGATCCTGAGAAAGCTGTGAGATGTTGAT 240
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
241 GAAACACACTATTGTGTGGCTGCTAICTTGGGTCCACCTCAATGGTGAATTTGAAGAT 300
221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
301 GTTAAGCGTTTAAATGACCTCTTGAATTGAGAAAAATGCCAAGACCGGATGGATACACCT 360
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
361 ATTCAATGTGACCGTGCAGTGCAGTGGTATTATTCGACCATTTATTTACCGGAACTTGAA 420
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysValTrpGlyLeu 280
421 TGGGATTTCCGGTTCGCATCTGGTGAAGAGTAAATGTTAGTGTACAAATATGGGCTT 480
281 ValTrpAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeu 300
481 GTTTACCGCGAATTGGTGGTGGTCAATTCGAGGAACAAGATGACATTCCTGATGAATC 540
301 IlePheHisIleAsnThrLeuGlyValAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
541 ATCTTTCCATCACTATCTTGGTGTGATCAACCAACTTCACTCTCAACTTCTCCAAA 600
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
601 GGTTCTAGTCAACAATGCTCAACTATCACTATCACTTCATTCGCTTGGGTTTCGAGGGATAC 660
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
661 AAGAGCATCATGGAAGAACTGTCAAGAAAATGCAAAATGTTCTAAAGAAAGGTTTGGAGAAA 720
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValPro 374
721 ACCGGAGGGTCAACATCATCTCTTAAAGACAACGGGGTCCCA 762

RESULT 10
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OCUS
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  arboreum cDNA clone GA_Ea0034H22f, mRNA sequence.
CCRESSION
  BE054156
EYWORDS
  EST.
SOURCE
  BE054156.2 GI:13246539
  Gossypium arboreum
  Gossypium arboreum
  Gossypium arboreum
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
  1; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
  (bases 1 to 803)
AUTHORS
  Wing R.A., Frisch D., Yu Y., Main D., Rambo T., Simmons J., Henry
  D., Wood T.C., Leslie A. and Wilkins T.A.
  An integrated analysis of the genetics, development, and evolution
  of the cotton fiber
  Unpublished
  On Jun 8, 2000 this sequence version replaced gi:8381212.
  Contact: Wing RA
  Clemson University Genomics Institute
  Clemson University
  100 Jordan Hall, Clemson, SC 29634, USA
  Tel: 864 656 7288
  Fax: 864 656 4293
  Email: rwing@clemson.edu
  Seq primer: TAATACACTCATATAGG
  High quality sequence stop: 792.
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    /mol_type="mRNA"
FEATURES
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/tissue_type="Fibers isolated from bolls harvested 7-10
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/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/notes="Vector: pBK-CMV; Site 1: EcoRI; Site 2: XhoI"
BASE COUNT 236 a 152 c 215 g 198 t 2 others
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  Score: 1196.00 Matches: 220
  Percent Similarity: 92.86% Conservative: 27
  Best Local Similarity: 82.71% Mismatches: 19
  Query Match: 45.74% Indels: 0
  DB: 10 Gaps: 0
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Db 2 GGGACAGTTGGTTCTCTGAGGCAATTAATGCTGCAGGATTAGCCTTTAAAGGAAGTGG 61
QY 142 GlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGlyAla 161
Db 62 CAACAAAAGATGAATCACAGGAAACCCGATGATGAATGAAGCCTAACATAGTCACCGGAGCG 121
QY 162 AsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGluVal 181
Db 122 AATGTGCAAGTGTGTGGAGAGCTTTGCGAGGATTTTCGAGGTTGAATGAAGGAAGT 181
QY 182 LysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAspGlu 201
Db 182 AAGTTGAAGAGGATACTATGATGACCTGTGAAGCGGTTGAAATGTTGACGAG 241
QY 202 AsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAspVal 221
Db 242 AATACCATATGTGTGACGAATTTCTGGATCCACCTTAACAGGGAGTTTGAGAAATGTG 301
QY 222 LysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrProIle 241
Db 302 AAGTCTCTTAATGAACCTTCTCACCAGAAGAAATGAAGAAACCGGTTGGGATACCCCAATA 361
QY 242 HisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGluTrp 261
Db 362 CATGTGGATGCTGCTAGTGGAGGGTTCATTGCTCTCTTGTACCCGAAATCGAATGG 421
QY 262 AspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeuVal 281
Db 422 GATTTCCGCTCGCGTTAGTAAAAAGCATCAATGTCAGTGGGCAAGATATGGCTTGTA 481
QY 282 TyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeuIle 301
Db 482 TATGCTGTATCGGTGGTGGTGTGGAGAAAGGAGGATTTGCCAGACGATCTCGTA 541
QY 302 PheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLysGly 321
Db 542 TTTCACATCAACTACCTTGGATCCGATCCAGCCACATTCACCTTANACTTCTCTAAAGGC 601
QY 322 SerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyrArg 341
Db 602 TCTAGTCAATCATAGTCAATATTATCAGCTTATTCGGCTCGGCTTNTGAGGGATACAAG 661
QY 342 AsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLysThr 361
Db 662 AGTATCATGGAAATTCATCGGGAATGCAAGAAATCTGAAGGAAGGATGATAAAAAACG 721
QY 362 GluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLys 381
Db 722 GGACGATTGGAAGTCGTCCTCAAGACGCTGGCGCTTCCCTCGGGGCTTTTGCTCTAAA 781

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382 AspSerSerCysHisThr 387
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 782 GACAGCACTAAATACACG 799

RESULT 11

UO023643

LOCUS 750 bp mRNA linear EST 23-AUG-2002
 QHG7H16.yg.ab1 OH EFGHJ sunflower RHA280 Helianthus annuus cDNA
 clone QHG7H16, mRNA sequence.

UO023643

UO023643.1 GI:22459163

EST:

Helianthus annuus (common sunflower)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.

1 (bases 1 to 750)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
 P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

REFERENCE

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Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

belongs to contig OH_CA_Contig2686, see http://cgdb.ucdavis.edu/

for details.

Plate: QHG7H16 row: C column: 03.

FEATURES

source

Location/Qualifiers

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/organism="Helianthus annuus"

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TAG_SEQ-Not found"

221 a 132 c 187 g 210 t

RIGIN

Alignment Scores:

Score: 1.04e-127 Length: 750

Percent Similarity: 1189.00 Matches: 221

Conservative: 94.80% Conservatives: 16

Mismatch: 88.40% Mismatches: 13

Query Match: 45.47% Indels: 0

DB: 13 Gaps: 0

US-10-006-852-2 (1-502) x UO023643 (1-750)

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QY 141 TrpGlnAsnLysArgLysAlaGluGlySerProValAspLysProAsnIleValThrGly 160

Db 61 TGGCAAAACAAATGAAAGCTCTTTGGCAAACTTTGGGACAAACCTAACTGTAAACCGGG 120

QY 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180

Db 121 GCCAACGTTTCAAGTTTGTGGAGAAATTTGCTCGGTATTTTGAAGTGGAGTTGAAGAA 180

QY 181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200

Db 181 GTGAAGTTTGGAGGAAGTTACTAGCTGATGATGATGATGATGATGATGATGATGATGAT 240

QY 201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220

Db 241 GAAACACTATTGTGTGGCTGCTATCTTTGGGTTCCACCTCAATGGTGAATTTGAAGAT 300

QY 221 ValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240

Db 301 GTTAAGCGTTTAAATGACCTCTTGATTGAGAAATGCCAAGACCGGATGGATACACCT 360

QY 241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaPropheLeuTyrProGluLeuGlu 260

Db 361 ATTCATGTGGACCGCTGCAAGTGGAGTTTATTGACCATTTATTACCCGGAATTTGAA 420

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QY 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340

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QY 341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlyLys 360

Db 661 AAGACATCATGGAATACTGTCAGAAATGCCAATGTTCTAAGAAAGGTTTGAGAAA 720

QY 361 ThrGluArgPheAsnIleValSerLysAsp 370

Db 721 ACCGACGGGTCAACATCATCTCTAAAGAC 750

RESULT 12

UO027739

LOCUS 786 bp mRNA linear EST 23-AUG-2002

QHG7H16.yg.ab1 OH EFGHJ sunflower RHA280 Helianthus annuus cDNA

clone QHG7H16, mRNA sequence.

UO027739

UO027739.1 GI:22463259

EST:

Helianthus annuus (common sunflower)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asterids; campanulids; Asterales; Asteraceae; Asteroideae;

Heliantheae; Helianthus.

1 (bases 1 to 786)

Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,

Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison

P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,

Church, S., Jackson, L. and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project

http://compgenomics.ucdavis.edu/

Unpublished

Contact: Alexander Kozik [R.W.Michelmore]

Department of Vegetable Crops, R.W.Michelmore Lab

University of California at Davis (UCD)

TITLE

JOURNAL

COMMENT

Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozikeatgc.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig QH_CA_Config2686, see <http://cgdb.ucdavis.edu/>
 for details.
 Plate: QHG7 row: H column: 16.

FEATURES

source

Location/Qualifiers
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 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="RHA280"
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 /clone_lib="QH_EFGHJ sunflower RHA280"
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 TAG TISSUE=hulls
 TAG SEQ=GCTAGTCGGG"

228 a

194 g

220 t

2 others

ALIGNMENT

Alignment Scores:

red. No.: 1.67e-127 Length: 786
 core: 1187.50 Matches: 227
 percent Similarity: 92.37% Conservative: 15
 best Local Similarity: 86.64% Mismatches: 18
 query Match: 45.41% Indels: 2
 B: 13 Gaps: 1

S-10-006-852-2 (1-502) x BU027739 (1-786)

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 1 GTTGGAACTGGGCTCATCGAAGCCATCATGTGGCGGAGTAGCTTCAAAAGAAA 60
 141 TrpGlnAsnLysArgLysAlaGluGlyProValAspLysProAsnIleValThrGly 160
 61 TGGCAAAACAAATGAAGCTCTTGGCAACCTTGGGACAACTTAACATTGTAAACGGG 120
 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
 121 GCCAACGTTCAAGTTGTGGGAGAAATTTGCTCGGTATTTTGAAGTGGAGTTGAAGGAA 180
 181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
 181 GTGAAGTTGAGGAGGTTACTACGTATGATGATGATGATGATGATGATGATGATGATGAT 240
 201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
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 Db 541 ATCTTTTCACTCAACTATCTTGGTGGTCAATCACTTCACTTCACTTCACTTCCAA 600
 QY 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeu-GlyHisGluGlyTy 340
 Db 601 GGTTCAGTCAATAATTTGCTCAATCTATCAGTTTCAGTTTCAGTTCGAGGGATA 660
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 ACCESSION
 BU025264
 VERSION
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 KEYWORDS
 EST.
 SOURCE
 Helianthus annuus (common sunflower)
 ORGANISM
 Helianthus annuus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; campanulids; Asterales; Asteraceae; Asteroideae;
 Heliantheae; Helianthus.
 REFERENCE
 1 (bases 1 to 746)
 Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
 Lin, H., van Damme, M., Lavalle, D., Chevalier, P., Ziegler, J., Ellison
 P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
 Church, S., Jackson, L. and Bradford, K.
 Lettuce and Sunflower ESTs from the Compositae Genome Project
 http://compgenomics.ucdavis.edu/
 Unpublished
 Contact: Alexander Kozik [R.W.Michelmore]
 Department of Vegetable Crops, R.W.Michelmore Lab
 University of California at Davis (UCD)
 Asmundson Hall, UCD, Davis, CA 95616, USA
 Tel: 1-(530)-742-1742
 Fax: 1-(530)-752-9659
 Email: akozikeatgc.org [michelmore@vegmail.ucdavis.edu]
 belongs to contig QH_CA_Config2686, see <http://cgdb.ucdavis.edu/>
 for details.
 Plate: QHF8 row: J column: 20.
 Location/Qualifiers
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 /organism="Helianthus annuus"
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 /cultivar="RHA280"
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 /note="Vector: pBRCDNASfiAB; The library was constructed from 11 different sources of RNA from a single genotype. Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated, directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library

construction can be obtained at <http://cgdb.ucdavis.edu/>
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TAG TISSUE=hulls
TAG SEQ=GCTAGTCGGG"

BASE COUNT 219 a 131 c 185 g 211 t
RIGIN

Alignment Scores:

red. No.: 3,01e-127 Length: 746
core: 1185.00 Matches: 220
Percent Similarity: 95.16% Conservative: 16
Best Local Similarity: 88.71% Mismatches: 12
Query Match: 45.32% Indels: 0
B: 13 Gaps: 0

US-10-006-852-2 (1-502) x BU025264 (1-746)

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b 1 GTTGGAACTGTGGCTCATCCGAAGCCATCATGTGGCGGACTAGCTTTCAAAAGAAAA 60
|||||
141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
|||||
b 61 TGGCAAAACAATGAAGCTCTTGGCAAACTTGGGACAACTTAACATTGTAAACCGGG 120
|||||
161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
|||||
b 121 GCCAAGCTTCAGGTTTGTGGGAGAAATTTGCTCGGTATTTTGAAGTGAGATTGAAGAA 180
|||||
181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnAlaValAspMetValAsp 200
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b 181 GTGAAGTTGAGGAAGGTACTACGTGATGGATCCTGAGAAAGCTGTGAGATGGTTGAT 240
|||||
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
|||||
b 241 GAAAAACATATTTGTGTGGCTGCTACTTGGGTTCACCTCAATGGTGAATTTGAAGAT 300
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221 ValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
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b 301 GTTAAAGCGTTTAAATGACCTCTTGAATGAGAAAAATGCCAAGACCGGATGGGATACACCT 360
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241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
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b 361 ATTCAATGTGACGCTCAAGTGAGGATTTTATTGCCACCAATTAATACCGGAACTTGA 420
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261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
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b 421 TGGGATTTCCGGTTGCCATTGGTTAAGAGTATAATGTTAGTGGTCACAAATATGGCTT 480
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281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300
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b 481 GTTTACCGCGAATTGGGTGGGTCAATTTGGAGGAACAAGATGACITTCCTGATGAATC 540
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301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
|||||
b 541 ATCTTTCAATCACTAATCTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 600
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321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
|||||
b 601 GGTTCTAGTCAAAATTAATGCTCAATATCATCATTCATTTCGCTTGGTTTCGAGGGATAC 660
|||||
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
|||||
b 661 AAGACATCATGGAATACTGTCAAGAAAAATGCAAAATGTTCTTAAGAAAGGTTTGGGAAA 720
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|||||
b 721 ACCGAGCGTTCAACATCATCTCT 744
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RESULT 14

BU027680

LOCUS

DEFINITION QHG7B13.yg.ab1 QH_EFGHJ sunflower RHA280 Helianthus annuus cDNA

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

clone QHG7B13, mRNA sequence.

BU027680

BU027680.1 GI:22463200

EST.

Helianthus annuus (common sunflower)

REFERENCE

Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lal,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>

AUTHORS

1 (bases 1 to 746)

Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lal,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
<http://compgenomics.ucdavis.edu/>

Unpublished

TITLE

Contact: Alexander Kozik [R.W.Michelmore]

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Asmundson Hall, UCD, Davis, CA 95616, USA

Tel: 1-(530)-742-1742

Fax: 1-(530)-752-9659

Email: akozik@ucdavis.edu [michelmore@vegmail.ucdavis.edu]

belongs to contig QH_CA.Contig2686, see <http://cgdb.ucdavis.edu/>

for details.

Plate: QHG7 row: B column: 13.

Location/Qualifiers

FEATURES

Source

1, 746

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/mol_type="mRNA"

/cultivar="RHA280"

/db_xref="taxon:4232"

/clone="QH7B13"

/lab_host="E.coli"

/note="Vector: pERCNAsfIAB; The library was constructed

from 11 different sources of RNA from a single genotype.

Separate cDNAs were generated using primers that

incorporated unique 5' and 3' tags to distinguish each

source of RNA. cDNAs were then pooled, size-fractionated,

directionally cloned into a custom medium-copy vector and

transformations made with four size classes to minimize

size bias. Details of each source of RNA and library

construction can be obtained at <http://cgdb.ucdavis.edu/>

TAG LIB=QH_EFGHJ sunflower RHA280

TAG TISSUE=hulls

TAG_SEQ=GCTAGTCGGG"

BASE COUNT 219 a 131 c 185 g 211 t

ORIGIN

Alignment Scores:

Pred. No.: 3,01e-127 Length: 746

Score: 1185.00 Matches: 220

Percent Similarity: 95.16% Conservative: 16

Best Local Similarity: 88.71% Mismatches: 12

Query Match: 45.32% Indels: 0

DB: 13 Gaps: 0

US-10-006-852-2 (1-502) x BU027680 (1-746)

QY

121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140

Db

1 GTTGGAACTGTGGCTCATCCGAAGCCATCATGTGGCGGACTAGCTTTCAAAAGAAAA 60

QY

141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160

Db

61 TGGCAAAACAATGAAGCTCTTGGCAAACTTGGGACAACTTAACATTGTAAACCGGG 120

QY

161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180

Db

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FEATURES		Location/Qualifiers	
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		TAG_L1B-QH_EFGHJ sunflower RHA280	
		TAG_SEQ=nulls	
		TAG_SEQ=GCTAGTCGGG	
BASE COUNT		218 a 132 c 185 g 211 t	
ORIGIN			
Alignment Scores:			
Pred. No.:		3.94e-127 Length: 746	
Score:		1184.00 Matches: 220	
Percent Similarity:		95.16% Conservative: 16	
Best Local Similarity:		88.71% Mismatches: 12	
Query Match:		45.28% Indels: 0	
DB:		13 Gaps: 0	
US-10-006-852-2 (1-502) x BU025649 (1-746)			
QY	121	ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys	140
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Db	61	TGGCAAAACAAATGAAAGCTCTTGGCAAACTTGGGACAAACCTAACATTGTAAACCGGG	120
QY	161	AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu	180
Db	121	GCAACAGTTTCAGTTTGTGGGAGAAATTCGTCGTATTGAGTGGAGTTGAAGAA	180
QY	181	ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp	200
Db	181	GTGAAGTTGAGGGAAGTTACTACGTGATGGATCCTGAGAAAGCTGTGGAGATGTTGAT	240
QY	201	GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp	220
Db	241	GAAACACATATTGTGTGGCTGCTACTTGTGGGTTCACCCCTCAATGGTGAATTTGAAAGAT	300
QY	221	ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro	240
Db	301	GTTAAGCGTTTAAATGACCTCTGATTGAGAAAAATGCCAGACCGGATGGATACACT	360
QY	241	IleHisValAspAlaAlaSerGlyGlyPheIleAlaPropheLeuTyrProGluLeuGlu	260
Db	361	ATTCAATGTGGACGCTGCAAGTGGAGTTTATTGACCACCATTTATTACCCGGAACCTGAA	420
QY	261	TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu	280
Db	421	TGGGATTTCCGGTTCATTTGTTAAGAGTATAAATGTTAGTGGTCACAAATATGGGCTT	480
QY	281	ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGluLeu	300
Db	481	GTTTACGCCGGAATTTGGGTGGGTTCATTTGGAGGACAAAGATGATTCCTCGATGAATC	540
QY	301	IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys	320
Db	541	ATCTTTACATCACTATCTTGGTCTGATCAACCACTTTTCACCTTCACTTCTCCAAA	600


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Y 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
b 601 GGTCTAGTCAAAATAATTGCTCAATACATATCAGTTCGCTTGGGTTTCGAGGATAC 660
Y 341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
b 661 AGAGCATCATGGGAAACTGTCAAGAAATGCAAAATGTTCTACAGAAAGTTTGGAGAA 720
Y 361 ThrGluArgPheAsnIleValSer 368
b 721 ACCGACGGTTCACATCATCTCT 744

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Search completed: October 22, 2003, 17:27:39
 Job time : 2452 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

MM protein - protein search, using sw model

run on: October 22, 2003, 14:50:13 ; Search time 69 Seconds
(without alignments)
1877.426 Million cell updates/sec

title: US-10-006-852-2
effect score: 2615
sequence: 1 MWLSHAVSESDVSVHSTFAS.....DIITGKKFVADRKKTSGIC 502

scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

searched: 830525 seqs, 258052604 residues

total number of hits satisfying chosen parameters: 830525

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

database : SPTREMBL.23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match %	Length	DB ID	Description
1	2240	85.7	496	10	O81102
2	2233	85.4	496	10	O81KR4
3	2232	85.4	496	10	P93369
4	2228	85.2	496	10	Q9AT17
5	2199	84.1	496	10	O81101
6	2191.5	83.8	513	10	O81LP2
7	2186.5	83.6	491	10	Q94KK8
8	2135.5	81.7	493	10	O92PS3
9	2126	81.3	494	10	Q944L6
10	2080	79.5	500	10	Q9ZPS4
11	2056.5	78.6	501	10	Q9AQU4
12	1969	75.3	494	10	O9LSH2
13	1965	75.1	494	10	O8LFR4
14	1845.5	70.6	419	10	O8RXH0
15	1844	70.5	500	10	Q9AP41
16	1321	50.5	520	3	Q8X0B0

17	1318	50.4	514	3	Q9UVD7	Q9uvd7 aspergillus
18	1251.5	47.9	467	16	P73043	P73043 synchocyst
19	1110	42.4	460	16	O06249	O06249 mycobacteri
20	1108	42.4	475	16	Q9X8J5	Q9x8j5 streptomyc
21	1100	42.1	468	17	Q8TPG4	Q8tpg4 methanosarc
22	1070.5	40.9	482	10	Q8RV54	Q8rv54 oryza sativ
23	1008	38.5	489	16	Q8FHG5	Q8fhg5 escherichia
24	1007.5	38.5	464	16	Q8XIO6	Q8xig6 clostridium
25	952	36.4	464	2	Q8GF15	Q8gf15 edwardsiell
26	635.5	24.3	304	16	Q8YBJ0	Q8ybj0 brucella me
27	613.5	23.5	177	10	Q9LSH6	Q9lsb6 arabidopsis
28	487	18.6	219	2	Q8L3L1	Q8l3l1 lactococcus
29	401	15.3	163	2	Q8L3L0	Q8l3l0 lactococcus
30	379	14.5	157	2	Q8LC52	Q8lc52 lactococcus
31	335.5	12.8	167	16	Q8YBI9	Q8ybi9 brucella me
32	325	12.4	589	3	Q05567	Q05567 saccharomyc
33	317	12.1	372	17	Q8TV92	Q8tv92 methanopyru
34	317	12.1	576	3	Q8X074	Q8x074 neurospora
35	314	12.0	384	17	Q9UZB5	Q9uzb5 pyrococcus
36	312	11.9	367	17	O27188	O27188 methanobact
37	311	11.9	367	17	O28275	O28275 archaeoglob
38	305	11.7	383	17	O58679	O58679 pyrococcus
39	299.5	11.5	545	5	Q9V7Y2	Q9v7y2 dirosophila
40	290.5	11.1	395	17	Q8TUQ9	Q8tuq9 methanosarc
41	288	11.0	552	5	Q9Y194	Q9y194 caenorhabdi
42	271	10.4	398	17	Q8PXA5	Q8pxa5 methanosarc
43	270	10.3	544	10	Q9C509	Q9c509 arabidopsis
44	269.5	10.3	488	17	O28946	O28946 archaeoglob
45	264.5	10.1	542	5	Q17456	Q17456 caenorhabdi

ALIGNMENTS

RESULT 1

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ID	O81102		
AC	O81102;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-OCT-2002 (TREMBLrel. 22, Last annotation update)		
DE	Glutamate decarboxylase isozyme 1.		
GN	NRGADI.		
OS	Nicotiana tabacum (Common tobacco).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;		
OC	Asteridae; lamids; Solanales; Solanaceae; Nicotiana.		
OX	NCBI_TaxID=4097;		
RN	[1]_TaxID=4097;		
RP	SEQUENCE FROM N.A.		
RA	Yun S.J., Oh S.H.;		
RT	"Cloning and characterization of a tobacco cDNA encoding		
RT	calcium/calmodulin-dependent glutamate decarboxylase.";		
RL	Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.		
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).		
CC	-I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).		
CC	EMBL; AF020425; AAC24195.1; -		
DR	InterPro: IPR002129; Pyridoxal dec.		
DR	Pfam: PF00282; pyridoxal dec; I.		
KW	Decarboxylase; Lyase; Pyridoxal phosphate.		
SQ	SEQUENCE 496 AA; 55963 MW; 4E8492F5DF0BDA8A CRC64;		

Query Match 85.7%; Score 2240; DB 10; Length 496;
Best Local Similarity 85.1%; Pred. No. 4.1e-161;
Matches 428; Conservative 35; Mismatches 32; Indels 8; Gaps 3;

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Db	1	MVLSKTASSDVSIHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDELMDGNPRLN 60
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b 61 ASFTVTWMEPCNKLMDS INKNYVDMDEYVPTTELQNCVNMIAHLFNAPLGDGETAVG 120
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181 VKLSDGYVMDPEKAVMDVENTICVAAIIGSTLNGEFEDVKLLNDLLIEKNKKTGMDTP 240
241 IHVDAASGGFTAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIWMWKNKEDLPEEL 300
241 IHVDAASGGFTAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIWMWKNKEDLPEEL 300
301 IFHNYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNWNCRENMIIVREGLEK 360
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361 TERPNIVSKDEGVLVAFSLKSSCHTEFEISDMRLRYGVWIVPAYTMPNAQHITVLRV 420
361 SGRFNIIISKEIGVPLVAFSLKDSQHNFEISETLRRFGWIVPAYTMPNAQHVTVLRV 420
421 IREDFSTLAERLVIDIEKVMRELDELPSRVHKKISLGOEKSESNSDNLMTVTKSDIDK 480
421 IREDFSTLAERLVIDIEKVLHEDTLPARNAKLAV---AANGSGVH--KKTREV 473
481 QDIITGWKKFVAD-RKXTSGIC 502
474 QLEITTAWKKFVADKKKKTNGVC 496

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RESULT 2

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D Q8LKR4 PRELIMINARY; PRT; 496 AA.
C Q8LKR4;
T 01-OCT-2002 (TReMBLrel. 22, Created)
T 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
T 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
E Glutamate decarboxylase.
S Nicotiana tabacum (Common tobacco).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
C Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
X NCBI_TaxID=4097;
N [1]
P SEQUENCE FROM N.A.
C STRAIN=cv. Samsun NN;
A McLean M.D., Yevtushenko D., Deschene A., Van Cauwenberghes O.R.,
A Makhmoudova A., Potter J.W., Bown A.W., Shelp B.J.;
T "Transgenic tobacco plants overexpressing glutamate decarboxylase are
T resistant to the root-knot nematode.";
L Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
C -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
C -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
C EMBL; AF506366; AAM48129.1; -
R InterPro; IPR002129; Pyridoxal dec.
R Pfam; PF00282; pyridoxal dec; I.
W Decarboxylase; Lyase; Pyridoxal phosphate.
Q SEQUENCE 496 AA; 55966 MW; 4771CF71BCA478349 CRC64;

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Query Match 85.4%; Score 2233; DB 10; Length 496;
Best Local Similarity 84.9%; Pred. No. 1.4e-160;
Matches 427; Conservative 35; Mismatches 33; Indels 8; Gaps 3;

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b 1 MVLSKTASESDVSHSTFASRYVTSLPRFKWPENSIKPEAAAYQIINDELMLDGNPRLN 60
Y 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYVPTTELQNCVNMIAHLFNAPLEAEATVG 120
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Db 121 VGTGSSSEAIMLAGLAFKRKWKQNKRAEGKPDVDPKPNITVGANVQVCWEKFARYFEVELKE 180
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Db 181 VKLSDGYVMDPEKAVMDVENTICVAAIIGSTLNGEFEDVKLLNDLLIEKNKKTGMDTP 240
QY 241 IHVDAASGGFTAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIWMWKNKEDLPEEL 300
Db 241 IHVDAASGGFTAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIWMWKNKEDLPEEL 300
QY 301 IFHNYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNWNCRENMIIVREGLEK 360
Db 301 IFHNYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNWNCRENMIIVREGLEK 360
QY 361 TERPNIVSKDEGVLVAFSLKSSCHTEFEISDMRLRYGVWIVPAYTMPNAQHITVLRV 420
Db 361 SGRFNIIISKEIGVPLVAFSLKDSQHNFEISETLRRFGWIVPAYTMPNAQHVTVLRV 420
QY 421 IREDFSTLAERLVIDIEKVMRELDELPSRVHKKISLGOEKSESNSDNLMTVTKSDIDK 480
Db 421 IREDFSTLAERLVIDIEKVLHEDTLPARNAKLAV---AANGSGVH--KKTREV 473
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Db 474 QLEITTAWKKFVADKKKKTNGVC 496

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RESULT 3

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AC P93369;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Glutamate decarboxylase.
GN NIGAD1.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Xanthi;
RA Dharmasiri M.A.N., Lu Y.T., Harrington H.M.;
RT "Cloning and sequencing of a tobacco cDNA encoding glutamate
RT decarboxylase.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
DR EMBL; U54774; AAB40608.1; -
DR InterPro; IPR002129; Pyridoxal dec.
DR Pfam; PF00282; pyridoxal dec; I.
KW Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 496 AA; 56035 MW; C48492F4BF0BDA8A CRC64;

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Query Match 85.4%; Score 2232; DB 10; Length 496;
Best Local Similarity 84.9%; Pred. No. 1.6e-160;
Matches 427; Conservative 35; Mismatches 33; Indels 8; Gaps 3;

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Db 1 MVLSKTASESDVSHSTFASRYVTSLPRFKWPENSIKPEAAAYQIINDELMLDGNPRLN 60
QY 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYVPTTELQNCVNMIAHLFNAPLEAEATVG 120
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QY 121 VGTGSSSEAIMLAGLAFKRKWKQNKRAEGKPDVDPKPNITVGANVQVCWEKFARYFEVELKE 180

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181 VKLSDGYVMDPEKAVEMVDENTICVAAAILGSTLNGEFEDVKRLNDLLIEKQKGTGWDTP 240
241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSGHKYGLVYAGIGWVWRNKEDLPDEL 300
241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSGHKYGLVYAGIGWVWRNKEDLPDEL 300
301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
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361 SGRFNIISKEIGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNNAQHTVLRVW 420
421 IREDFSRTLAERLVIDIEKVMRELDELPSRVIHKISLGOEKSESNDLMTVTVKSDIDK 480
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481 QRDITGWKKFVAD-RKKTSGIC 502
474 QLEITAAWKKFVADKKKKTNGVC 496

RESULT 4
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D 09AT17
T 01-JUN-2001 (TREMREL. 17, Created)
T 01-JUN-2001 (TREMREL. 17, Last sequence update)
T 01-OCT-2002 (TREMREL. 22, Last annotation update)
E Glutamate decarboxylase isozyme 3 (EC 4.1.1.15).
S Nicotiana tabacum (Common tobacco).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
C Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
X NCBI_TaxID=4097;
P SEQUENCE FROM N.A.
N STRAIN=cv. Samsun NN;
A Yevtushenko D., McJean M.D., Peiris S.B., Van Cauwenberghe O.R.,
A Shelp B.J.;
T "Two isoforms of tobacco glutamate decarboxylase are regulated by
T calcium/calmodulin and differ in organ distribution.";
L Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
C -|- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
C -|- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, HDC AND
C TYRDC).
R EMBL; AF352732; AAK18620.1; -.
R InterPro; IPR002129; Pyridoxal_dec.
R Pfam; PF00282; pyridoxal dec; 1.
W Decarboxylase; Lyase; Pyridoxal phosphate.
Q SEQUENCE 496 AA; 55875 MW; CC61BCD3531827BB CRC64;

Query Match 85.2%; Score 2228; DB 10; Length 496;
Best Local Similarity 84.7%; Pred. No. 3.3e-160;
Matches 426; Conservative 35; Mismatches 34; Indels 8; Gaps 3;

Y 1 MYLSHAVSESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDEMLDGNPRNL 60
b 1 MYLSKTASESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDEMLDGNPRNL 60
Y 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEATVG 120
b 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEATVG 120
Y 121 VGTGSSSEALMAGLAFKRWQKMAQKPCDKPNIVTGANVQVCWEKFARYFEVELKE 180
b 121 VGTGSSSEALMAGLAFKRWQKMAQKPCDKPNIVTGANVQVCWEKFARYFEVELKE 180
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QY 181 VKLSEGYVMDPQOAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKQKGTGWDTP 240
Db 181 VKLSDGYVMDPEKAVEMVDENTICVAAAILGSTLNGEFEDVKRLNDLLIEKQKGTGWDTP 240
QY 241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSGHKYGLVYAGIGWVWRNKEDLPDEL 300
Db 241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSGHKYGLVYAGIGWVWRNKEDLPDEL 300
QY 301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
Db 301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
QY 361 TERFNIVSKDGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNNAQHTVLRVW 420
Db 361 SGRFNIISKEIGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNNAQHTVLRVW 420
QY 421 IREDFSRTLAERLVIDIEKVMRELDELPSRVIHKISLGOEKSESNDLMTVTVKSDIDK 480
Db 421 IREDFSRTLAERLVIDIEKVMRELDELPSRVIHKISLGOEKSESNDLMTVTVKSDIDK 480
QY 481 QRDITGWKKFVAD-RKKTSGIC 502
Db 474 QLEITAAWKKFVADKKKKTNGVC 496

RESULT 5
081101 PRELIMINARY; PRT; 496 AA.
AC 081101,
DT 01-NOV-1998 (TREMREL. 08, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DT 01-OCT-2002 (TREMREL. 22, Last annotation update)
DE Glutamate decarboxylase isozyme 2.
GN NTGAD2.
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98302498; PubMed=9638642;
RA Yun S.J., Oh S.H.;
RT "Cloning and characterization of a tobacco cDNA encoding
RT calcium/calmodulin-dependent glutamate decarboxylase.";
RL Mol. Cells 8:125-129(1998).
CC -|- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, HDC AND
CC TYRDC).
DR EMBL; AF020424; AAC39483.1; -.
DR InterPro; IPR002129; Pyridoxal_dec.
DR Pfam; PF00282; pyridoxal dec; 1.
KW Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 496 AA; 55931 MW; 5B9D2C8E12560D27 CRC64;

Query Match 84.1%; Score 2199; DB 10; Length 496;
Best Local Similarity 84.1%; Pred. No. 5.2e-158;
Matches 423; Conservative 34; Mismatches 38; Indels 8; Gaps 3;

QY 1 MYLSHAVSESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDEMLDGNPRNL 60
Db 1 MYLSKTASESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDEMLDGNPRNL 60
QY 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEATVG 120
Db 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEATVG 120
QY 121 VGTGSSSEALMAGLAFKRWQKMAQKPCDKPNIVTGANVQVCWEKFARYFEVELKE 180
Db 121 VGTGSSSEALMAGLAFKRWQKMAQKPCDKPNIVTGANVQVCWEKFARYFEVELKE 180
QY 181 VKLSEGYVMDPQOAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKQKGTGWDTP 240
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181 VKLSGGYVMDPKAVEMVDENTICVAAILGSLTNGEFEDVRLNDLLIEKNKETGWDTP 240
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSQHYGLVAGIGWVWRNKEDLPBEL 300
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSQHYGLVAGIGWVWRNKEDLPBEL 300
301 IFHINYLGDQPTFTNFKSGSQVIAQYQIRLIRLHGHYRNVMNCNRMIVLREGLEK 360
301 IFHINYLGDQPTFTNFKSGSQVIAQYQIRLIRLHGHYRNVMNCNRMIVLREGLEK 360
361 TERFNIVSKDEGVLPAFSLKSSCHTEFEISDMLRYGVIWPAVMPNAOHIIVLRVV 420
361 SGFNLSKEIGVPLVAFSLKSSCHTEFEISDMLRYGVIWPAVMPNAOHIIVLRVV 420
421 IREDFSRITLAERLVIDIEKVMRELDLPSRVIHKISLGOEKSESNDNLMVTVKSDIDK 480
421 IREDFSRITLAERLVIDIEKVMRELDLPSRVIHKISLGOEKSESNDNLMVTVKSDIDK 480
481 QRDIIITGKKFVAD-RKKTSGIC 502
474 QLEITTAWLKFEVADKKKTNGVC 496

RESULT 6
BLP2
D Q8LLP2 PRELIMINARY; PRT; 513 AA.
C Q8LLP2;
I 01-OCT-2002 (TrEMBLrel. 22, Created)
T 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
E 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
E Putative glutamate carboxylase.
S OSJNB0031009.06.
S Oryza sativa (japonica cultivar-group).
N Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
C Ehrhartoideae; Oryzeae; Oryza.
X NCBI_TaxID=39947;
N [1]
N SEQUENCE FROM N.A.
P Eastman A.P., Smith S.C., Bertin N., Liang C., Gingle A.R.,
A Pratt L.H., Cordonnier-Pratt M.-M.;
A "Sequencing of clone OSJNB0031009.";
T Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
L [2]
N SEQUENCE FROM N.A.
P Eastman A.P., Smith S.C., Bertin N., Liang C., Najjar F.Z., Pratt L.H.,
A Cordonnier-Pratt M.-M.;
A "Untitled.";
T Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
L [3]
C -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
C -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
C EMBL; AF377946; AAM47304.1; -.
R Gramene; Q8LLP2; -.
R InterPro; IPR002129; Pyridoxal dec.
R Pfam; PF00282; Pyridoxal dec; 1.
R Decarboxylase; Lyase; Pyridoxal phosphate.
W Decarboxylase; Lyase; Pyridoxal phosphate.
Q SEQUENCE 513 AA; 57378 MW; 131DFD62F6B0CE87 CRC64;

Query Match 83.8%; Score 2191.5; DB 10; Length 513;
Best Local Similarity 79.7%; Pred. No. 2e-157;
Matches 417; Conservative 38; Mismatches 37; Indels 31; Gaps 2;

1 MVLHSHVSDSVSHSTFASRYVTSLSR-----FKMPENSIPK 39
1 MVLHSHVSGSDSVSHSTFASRYVTSLSRPHARGPLSRAPLAPIDSVIDWEFRMQSIPK 60
40 EAAVQIINDELMIDGNPRNLASPTVTWMEPCDKLIMSSINKNVYMDDEYPTTTELQNR 99
61 EAAVQIINDELMIDGNPRNLASPTVTWMEPCDKLIMSSINKNVYMDDEYPTTTELQNR 120
100 CVNMIAHLFNAPLEAEATAVGVGTGSSSEAIMLAGLAFKRWQNKKAEGKPVDPKXNIVT 159
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Db 121 CVNMIAHLFNAPLGDSSTAVGVGTGSSSEAIMLAGLAFKRWQNKKAAGKPCDKPNIVT 180
QY 160 GANVOVCWEKFARFEVELKEVLSGGYVMDPKAVEMVDENTICVAAILGSLTNGEFE 219
Db 181 GANVOVCWEKFARFEVELKEVLSGGYVMDPKAVEMVDENTICVAAILGSLTNGEFE 240
QY 220 DVKLLNDLLIEKNKETGWDTPIHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSQHYK 279
Db 241 DVKLLNDLLIEKNKETGWDTPIHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSQHYK 300
QY 280 LVYAGIGWVWRNKEDLPBELIHINYLGDQPTFTNFKSGSQVIAQYQIRLIRLHGHG 339
Db 301 LVYAGIGWVWRNKEDLPBELIHINYLGDQPTFTNFKSGSQVIAQYQIRLIRLHGHG 360
QY 340 YRNVMNCNRMIVLREGLEKTERFNIVSKDEGVLPAFSLKSSCHTEFEISDMLRYG 399
Db 361 YRNVMNCNRMIVLREGLEKTERFNIVSKDEGVLPAFSLKSSCHTEFEISDMLRYG 420
QY 400 WIVPAYTMPNAOHIIVLRVIREDFSRITLAERLVIDIEKVMRELDLPSRVIHKISLGO 459
Db 421 WIVPAYTMPNAOHIIVLRVIREDFSRITLAERLVIDIEKVMRELDLPSRVIHKISLGO 473
QY 460 EKSESNDNLMVTVKSDIDKQRDIIITGKKFVADRKKTSGIC 502
Db 474 ---ANGGDAAAASASEREMEKQREVISLWKAVALAKKTNGVC 513

RESULT 7
Q94KK8
ID Q94KK8 PRELIMINARY; PRT; 491 AA.
AC Q94KK8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Glutamate decarboxylase isozyme 4 (EC 4.1.1.15).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxID=4097;
RN [1]
RP SEQUENCE FROM N.A.
RA Yervushenko D., McLean M.D., Peiris S.E., Van Cauwenbergh O.R.,
RA Shelp B.J.;
RT "Two isoforms of tobacco glutamate decarboxylase are regulated by calcium/calmodulin and differ in organ distribution.";
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
CC -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
CC EMBL; AF353615; AAK38667.1; -.
DR InterPro; IPR002129; Pyridoxal dec.
DR Pfam; PF00282; Pyridoxal dec; 1.
DR Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 491 AA; 55950 MW; 51CB78B3EF3F4E35 CRC64;

Query Match 83.6%; Score 2186.5; DB 10; Length 491;
Best Local Similarity 84.9%; Pred. No. 4.5e-157;
Matches 421; Conservative 27; Mismatches 39; Indels 9; Gaps 1;

1 MVLHSHVSDSVSHSTFASRYVTSLSRPFKMPENSIPKGAAYOIINDELMIDGNPRNL 60
1 MVLKTSSESQSVSHSTFASRYVTSLSRPFKMAENSIPKGAAYOIINDELMIDGNPRNL 60
61 ASFVTTWMEPCDKLIMSSINKNVYMDDEYPTTTELQNRQNVNMIHAFNAPLEAEATAVG 120
61 ASFVTTWMEPCDKLIMSSINKNVYMDDEYPTTTELQNRQNVNMIHAFNAPLEAEATAVG 120
121 VGTGSSSEAIMLAGLAFKRWQNKKAEGKPVDPKXNIVTGANVOVCWEKFARFEVELKE 180
121 VGTGSSSEAIMLAGLAFKRWQNKKAEGKPVDPKXNIVTGANVOVCWEKFARFEVELKE 180
181 VKLSGGYVMDPKAVEMVDENTICVAAILGSLTNGEFEDVRLNDLLIEKNKETGWDTP 240
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181 VKUREGYVNDPVOAVEMVDENTICVAAILGSLTNGEFEDVKLLNDLLTEKKNQOTGWNTP 240
|||||
241 IHVDAASGGFIAPFLYPELEWDFELPLVKSINVSCHKYGLVYAGIGWIVRNKEDLPPEEL 300
|||||
241 IHVDAASGGFIAPFLYPELEWDFELPLVKSINVSCHKYGLVYAGIGWIVRNKEDLPPEEL 300
|||||
301 IFHINVLGADQPTFTLNFSKSSQVIAQYQYQIRLGHGVRNVMNCNRMNIVLRGLBK 360
|||||
301 IFHINVLGADQPTFTLNFSKSSQVIAQYQYQIRLGHGVRNVMNCNRMNIVLRGLBK 360
|||||
361 TERFNIVSKDEGVPLVAFSLKDSCHTEREISDMLARYGWIIVPAYTMPNQAQHTVLRVV 420
|||||
361 TGRFNIVSKDEGVPLVAFSLKDSCHTEREISDMLARYGWIIVPAYTMPNQAQHTVLRVV 420
|||||
421 IRBDFSRITLAERLVIDIEKVMRDELPSRVIHKISLGQEKSESNDLMVTVKKSDIDK 480
|||||
421 IRBDFSRITLAERLVIDIEKVMRDELPSRVIHKISLGQEKSESNDLMVTVKKSDIDK 480
|||||
481 QRDITIGWKKFVADRK 496
|||||
472 QREVTYWKLL-ETKKTN 488
|||||

RESULT 8
92P53 PRELIMINARY; PRT; 493 AA.
C Q2P53
T 01-MAY-1999 (T-EMBLrel. 10, Created)
T 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
T 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
E Putative glutamate decarboxylase (AF2G02010/F14H20.8).
F F14H20.8.
S Arabidopsis thaliana (Mouse-ear cress).
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
C eurosids II; Brassicales; Brassicaceae; Arabidopsids.
X NCBI_TaxID=3702;
P [1]
N SEQUENCE FROM N.A.
C STRAIN=cv. Columbia;
A Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., VanAken S.E.,
A Barnstead M.E., Mason T.M., Bowman C.L., Rensing C.M., Benito M.,
A Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Niernan W.C.,
A Fraser C.M., Venter J.C.;
T "Arabidopsis thaliana chromosome II BAC F14H20 genomic sequence.";
T Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
P [2]
N SEQUENCE FROM N.A.
A Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
A Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y., Ishida J.,
A Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M.,
A Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
A Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M., Seki M.,
A Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K., Davis R.W.,
A Theologis A., Ecker J.R.;
T "Arabidopsis cDNA clones.";
T Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
P [3]
N SEQUENCE FROM N.A.
A Cheuk R., Chen H., Kim C.J., Shinn P., Banh J., Bowser L.,
A Carninci P., Chang E., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
A Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
A Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
A Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
A Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S.,
A Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
T "Arabidopsis ORF clones.";
T Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
N COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
EMBL; AC006532; AAB20099.1; -.
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DR EMBL; AF361836; AAK32848.1; -.
DR EMBL; AY124860; AAM70569.1; -.
DR InterPro; IPR002129; Pyridoxal dec.
DR Pfam; PF00282; pyridoxal dec; 1.
KW Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 493 AA, 56005 MW, 36B3FC93F2978168 CRC64;

Query Match 81.7%; Score 2135.5; DB 10; Length 493;
Best Local Similarity 82.4%; Pred. No. 3.3e-153;
Matches 411; Conservative 32; Mismatches 45; Indels 11; Gaps 2;

QY 1 MYLSHAVSESQVSVHSTFASKYVTRISLPRFKWPENSIPKEAAYQIINDELMDGNPNRL 60
DB 1 MYLSKTVSSEDSVSHSTFASKYVTRISLPRFKWPENSIPKEAAYQIINDELMDGNPNRL 60
QY 61 ASFVTTWMEPECDKLIMSINKNYVDMDEYPTVTELONRQVNMIAHFNAPLEEAETAVG 120
DB 61 ASFVTTWMEPECDKLIMSINKNYVDMDEYPTVTELONRQVNMIAHFNAPLEEAETAVG 120
QY 121 VGTGSSBAIMLAGLAPFRKQWQKKAESGKPVDPKNIVTGANVQVCWCKFARYFEVELKE 180
DB 121 VGTGSSBAIMLAGLAPFRKQWQKKAESGKPVDPKNIVTGANVQVCWCKFARYFEVELKE 180
QY 181 VKLSGGYVMDPQQAVDMVDENTICVADILGSLTNGEFEDVKLLNDLLVEKNKGTGMDTP 240
DB 181 VNLREDYVMDPEVKAVEMVDENTICVADILGSLTNGEFEDVKLLNDLLVEKNKGTGMDTP 240
QY 241 IHVDAASGGFIAPFLYPELEWDFELPLVKSINVSCHKYGLVYAGIGWIVRNKEDLPPEEL 300
DB 241 IHVDAASGGFIAPFLYPELEWDFELPLVKSINVSCHKYGLVYAGIGWIVRNKEDLPPEEL 300
QY 301 IFHINVLGADQPTFTLNFSKSSQVIAQYQYQIRLGHGVRNVMNCNRMNIVLRGLBK 360
DB 301 IFHINVLGADQPTFTLNFSKSSQVIAQYQYQIRLGHGVRNVMNCNRMNIVLRGLBK 360
QY 361 TERFNIVSKDEGVPLVAFSLKDSCHTEREISDMLARYGWIIVPAYTMPNQAQHTVLRVV 420
DB 361 TGRFNIVSKDEGVPLVAFSLKDSCHTEREISDMLARYGWIIVPAYTMPNQAQHTVLRVV 420
QY 421 IRBDFSRITLAERLVIDIEKVMRDELPSRVIHKISLGQEKSESNDLMVTVKKSDIDK 480
DB 421 IRBDFSRITLAERLVIDIEKVMRDELPSRVIHKISLGQEKSESNDLMVTVKKSDIDK 480
QY 481 QRDITIGWKKFVADRK 499
DB 471 QREVTYWKLL-ETKKTN 488

RESULT 9
Q944L6 PRELIMINARY; PRT; 494 AA.
AC Q944L6;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (T-EMBLrel. 22, Last annotation update)
DE Atg95960/F12P19-12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
RA Carninci P., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
RA Bowser L., Jones T., Jones T., Kamiya A., Karlin-Neumann G.,
RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
RA Ecker J.R.;
RT "Arabidopsis cDNA clones.";
RT Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
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T	01-JUN-2001 (TRENBLrel. 17, Created)	DT	01-OCT-2000 (TRENBLrel. 15, Created)
T	01-JUN-2001 (TRENBLrel. 17, Last sequence update)	DT	01-OCT-2000 (TRENBLrel. 15, Last sequence update)
T	01-OCT-2002 (TRENBLrel. 22, Last annotation update)	DT	01-OCT-2002 (TRENBLrel. 22, Last annotation update)
E	Glutamate decarboxylase (EC 4.1.1.15).	DE	Glutamate decarboxylase.
E	GAD.	OS	Arabidopsis thaliana (Mouse-ear cress).
S	Oryza sativa (Rice).	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
C	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
C	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;	OC	eusoids II; Brassicales; Brassicaceae; Arabidopsis.
C	Ehrhartoideae; Oryzeae; Oryza.	OX	NCBI_TaxID=3702;
X	NCBI_TaxID=4530;	RN	[1]
N	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
P	STRAIN=cv. Nipponbare; TISSUE=Shoot;	RC	STRAIN=Columbia;
C	Akama K., Akihiro T., Kitagawa M., Takaiwa F.;	RA	Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
A	"Molecular characterization of two genes encoding glutamate	RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
T	decarboxylase from rice (Oryza sativa).";	RN	[2]
L	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.	RP	SEQUENCE FROM N.A.
C	- - COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).	RC	STRAIN=Columbia;
C	- - SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND	RX	MEDLINE=20277480; PubMed=10819329;
C	TYRDC).	RA	Nakamura Y.;
R	EMBL; AB056062; BAB32870.1; -.	RT	"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
R	EMBL; AB056060; BAB32868.1; -.	RT	features of the regions of 4,504,864 bp covered by sixty P1 and TAC
R	Gramene; Q9AQU4; -.	RT	clones.";
R	InterPro; IPR002129; Pyridoxal dec.	RL	DNA Res. 7:131-135(2000).
R	Pfam; PF00282; pyridoxal dec. I.	CC	- - COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
R	Decarboxylase; Lyase; Pyridoxal phosphate.	CC	- - SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
W	SEQUENCE 501 AA; 56657 MW; E84962C147FFA7A8 CRC64;	CC	TYRDC).
Q		DR	EMBL; AB026646; BAB02870.1; -.
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b	Best Local Similarity 78.1%; Pred. No. 3.2e-147;	DR	Pfam; PF00282; pyridoxal dec. I.
b	Matches 395; Conservative 44; Mismatches 58; Indels 9; Gaps 4;	KW	Decarboxylase; Lyase; Pyridoxal phosphate.
Y	1 MVLSHAVSRSDD----VSVHSTFASRYVRSLSLPRFKWPENSIPKEAAYQIINDELMDGNP 56	SQ	SEQUENCE 494 AA; 55770 MW; 7985F175E54DF262 CRC64;
b	1 MVSVAAATSDTAQYQYQYFFASRYVRSLSLPRFKWPENSIPKEAAYQIINDELMDGNP 60	Qy	1 MVLHAVSESQVSVHSTFASRYVRSLSLPRFKWPENSIPKEAAYQIINDELMDGNPRLNL 60
Y	57 RNLASFVTTWMEPECDKLIIMSSINKNYVDMDEYPTVTELOQRCVNMIAHLFNAPLEAE 116	Db	1 MVLA--TNSDSDEHLHSTFASRYVRAVWPRFOPDPCPKDAAYQVINDELMDGNPRLNL 59
b	61 RNLASFVTTWMEPECDKLIIMDSVNKNYVDMDEYPTVTELOQRCVNMIAHLFNAPLEAE 120	Qy	61 ASFVTTWMEPECDKLIIMSSINKNYVDMDEYPTVTELOQRCVNMIAHLFNAPLEAEAVG 120
Y	117 TAVGVGTGVSSEAIMLAGLAFKRWQKRAEKGPVDKPNIVTGANVQVCWEKFARYFEV 176	Db	60 ASFVTTWMEPECDKLIIMDSVNKNYVDMDEYPTVTELOQRCVNMIAHLFNAPVGEDEAIG 119
b	121 TAVGVGTGVSSEAIMLAGLAFKRWQKRAEKGPVDKPNIVTGANVQVCWEKFARYFEV 180	Qy	121 VGTGSSSEAIMLAGLAFKRWQKRAEKGPVDKPNIVTGANVQVCWEKFARYFEVELKE 180
Y	177 ELKEVKLSEGYVMDPQQAQVMDVENTICVADILGSTLNGEFEDVKLLNDLLVERNKETG 236	Db	120 CQTGSSSEAIMLAGLAFKRWQKRAEKGPVDKPNIVTGANVQVCWEKFARYFEVELKE 179
b	181 ELKEVKLSEGYVMDPVKAVEMVDENTICVAAILGSTLTGTGEFEDVKLLNNLLTERKNK 240	Qy	181 VKLSGYYVMDPQQAQVMDVENTICVADILGSTLNGEFEDVKLLNDLLVERNKETGWDTP 240
Y	237 WDTPPIHVDAASGGFIAPFLYPELEWDFRPLVKSINVSCHKYGLVYAGIGWIRNKEDEL 296	Db	180 VKLSGYYVMDPAKAVEMVDENTICVAAILGSTLTGTGEFEDVKQNDLLAERKNAETGWETP 239
b	241 WDTPPIHVDAASGGFIAPFLYPELEWDFRPLVKSINVSCHKYGLVYAGIGWIRNKEDEL 300	Qy	241 IHVDAASGGFIAPFLYPELEWDFRPLVKSINVSCHKYGLVYAGIGWIRNKEDELPEEL 300
Y	297 PEELIHFHNYLGADQPTFTLNFSGSSQVIAQYQYQLIRLGHGEGYNNMNCNEMIVLRE 356	Db	240 IHVDAASGGFIAPFLYPELEWDFRPLVKSINVSCHKYGLVYAGIGWIRNKEDELPEEL 299
b	301 PEELIHFHNYLGADQPTFTLNFSGSSQVIAQYQYQLIRLGHGEGYNNMNCNEMIVLRE 360	Qy	301 IPHINYLGADQPTFTLNFSGSSQVIAQYQYQLIRLGHGEGYNNMNCNEMIVLREGLK 360
Y	357 GLBKTFRFNIVSKDEGVPVAVFSLKSSCHTEFEISDMLRRYGVIVPYPATMPNACHITV 416	Db	300 VPHINYLGADQPTFTLNFSGSSQVIAQYQYQLIRLGHGEGYNNMNCNEMIVLREGLK 359
b	361 GIEATGRFELSKAEGVPLVAFSLKSSGRYTVFDIISEHLRRFGWIVPYPATMPNASHAV 420	Qy	361 TERFNIVSKDEGVPVAVFSLKSSCHTEFEISDMLRRYGVIVPYPATMPNACHITVLRVV 420
Y	417 LRVVIRDFSRITLAERLVIDIEKVMRELDELPSRVHKLISLQEKSESNDLMVTVTKS 476	Db	360 TGFKNIVSKDVGVPVAVFSLKSSCHTEFEISDMLRRYGVIVPYPATMPNACHITVLRVV 419
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Y	477 DIDKQDIIITGKKFVADRKTGIC 502	Db	420 IREDFSRITLAERLVIDIEKVMRELDELPSRVHKLISLQEKSESNDLMVTVTKSIDX 475
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QC 09LSH2;			

Job time : 73 secs

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01-JUN-2001 (TREMELrel. 17, Last sequence update)
01-OCT-2002 (TREMELrel. 22, Last annotation update)
Glutamate decarboxylase (EC 4.1.1.15).
GAD.
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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NCBI_TaxID=4530;
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STRAIN=cv. Nipponbare; TISSUE=Shoot;
Akama K., Akihiro T., Kitagawa M., Takaiwa F.;
"Molecular characterization of two genes encoding glutamate
decarboxylase from rice (Oryza sativa).";
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
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EMBL; AB056063; BAB32871.1; -.
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Pfam; PF00282; pyridoxal dec. 1.
Decarboxylase; Lyase; Pyridoxal phosphate.
SEQUENCE 500 AA; 55615 MW; 0E19E61CCAD5F508 CRC64;

Query Match 70.5%; Score 1844; DB 10; Length 500;
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Matches 355; Conservative 56; Mismatches 81; Indels 18; Gaps 5;

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b 121 VGVGTGSSAIIAGLAFKRRKQNRKKAEGKVDKPNIVTGANVQVCWEKFPARYPEVEL 180
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b 181 KEVKLTGECVMDPVKAVDMVDENTICVAILGSTITGEFEDVRLNDLLAAKNKETGWD 240
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b 301 ELIPHINYLGNQDQFTFTNFSGSSQVIAQYQIILRGHEGYRNVKNCESARTLREGL 360
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b 361 EKTCRFTIISKEGVPLVATFTKDGAGAQAFRLSSGLRGRYGVIPVATPMPAALHNVTVR 420
Y 419 VVIREDFSRTLAEKLVIDIEKWNKELD-----ELPSRVTHKISLGOEKSESNDLMVTV 473
b 421 VVIREDFGRPLAEKLVIRVMALDENMDLAARAPVP-RVQLTIELGPARTAGEASIRVVK 479
Y 474 KKS-DIDKQRIILTGWKKFVADRKKTSIC 502
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.
October 22, 2003, 16:47:21 ; Search time 359 Seconds
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Total number of hits satisfying chosen parameters: 3584790
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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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2	2607	99.7	1509	10	US-09-338-842A-1810	Sequence 1810, Ap
3	2250	86.0	1785	14	US-10-006-852-15	Sequence 15, Appl
4	2240	85.7	1705	14	US-10-006-852-11	Sequence 11, Appl
5	2233	85.4	1745	14	US-10-005-602-1	Sequence 1, Appli
6	2200	84.1	1479	10	US-09-887-576-820	Sequence 820, App
7	2199	84.1	1771	14	US-10-006-852-13	Sequence 13, Appl
8	2135.5	81.7	1482	10	US-09-338-842A-937	Sequence 937, App
9	2130	81.5	1665	14	US-10-006-852-3	Sequence 3, Appli
10	2073	79.3	1497	12	US-10-167-547C-1	Sequence 1, Appli
11	2014	77.0	1783	14	US-10-006-852-17	Sequence 17, App
12	2007	76.7	1455	10	US-09-887-576-782	Sequence 782, App
13	1935.5	74.1	2121	14	US-10-006-852-7	Sequence 7, Appli
14	1895.5	72.3	1287	10	US-09-887-576-806	Sequence 806, App
15	1864	71.3	1530	12	US-10-167-547C-3	Sequence 3, Appli
16	1854	71.3	1590	12	US-10-167-547C-5	Sequence 5, Appli
17	1854	70.9	1467	10	US-09-887-576-777	Sequence 777, App
18	1836	70.2	1180	11	US-09-727-758-1	Sequence 1, Appli
19	1834.5	70.2	2493	14	US-10-006-852-5	Sequence 5, Appli
20	1782	68.1	1946	14	US-10-006-852-9	Sequence 9, Appli
21	1630	62.3	5160	10	US-09-887-576-443	Sequence 443, App
22	1314.5	50.3	1302	10	US-09-887-576-783	Sequence 783, App
23	1184	45.3	894	12	US-10-167-547C-30	Sequence 30, Appl
24	1082	41.4	1410	14	US-10-156-761-4639	Sequence 4639, Ap
25	1082	41.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
26	1051	40.2	1362	14	US-10-156-761-3588	Sequence 3588, Ap
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28	934	35.7	742	10	US-09-966-881-20	Sequence 20, Appl
29	851	32.5	807	10	US-09-966-881-21	Sequence 21, Appl
30	620.5	23.7	440	9	US-09-770-444-922	Sequence 922, App
31	545	20.8	387	10	US-09-878-574-1480	Sequence 1480, Ap
32	452	17.3	493	11	US-09-770-961-610	Sequence 610, App
33	438	16.7	280	10	US-09-878-574-7302	Sequence 7302, Ap
34	436.5	16.7	781	11	US-09-989-442-73	Sequence 73, Appl
35	347	13.4	277	10	US-09-878-574-13198	Sequence 13198, A
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42	265.5	10.2	1629	14	US-10-053-510-3	Sequence 3, Appli
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44	257	9.8	359	12	US-10-084-843-192	Sequence 192, App
45	257	9.8	359	12	US-10-193-002-187	Sequence 187, App

ALIGNMENTS

RESULT 1
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; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kinnersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006.852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 1
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1509)
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SB:	14	Gaps:	0						
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; Patent No. US20020160378A1									
; GENERAL INFORMATION:									
; APPLICANT: Harper, Jeff									
; APPLICANT: Kreps, Joel									
; APPLICANT: Wang, Xun									
; APPLICANT: Zhu, Tong									
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING									
; FILE REFERENCE: SCRIP1300-3									
; CURRENT APPLICATION NUMBER: US/09/938,842A									
; CURRENT FILING DATE: 2001-08-24									
; PRIOR APPLICATION NUMBER: US 60/227,866									
; PRIOR FILING DATE: 2000-08-24									
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; PRIOR FILING DATE: 2001-01-16									
; PRIOR APPLICATION NUMBER: US 60/300,111									
; PRIOR FILING DATE: 2001-06-22									
; NUMBER OF SEQ IDS NOS: 5379									
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 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE OF INVENTION: SAME, AND METHODS OF USE
 ; FILE REFERENCE: SCRI1300-3
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 1810
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 US-09-938-842A-1810
 Alignment Scores:
 Pred. No.: 6.94e-294 Length: 1509
 Score: 2607.00 Matches: 501
 Percent Similarity: 99.80% Conservative: 0
 Best Local Similarity: 99.80% Mismatches: 1

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ery Match: 99.69% Indels: 0 Gaps: 0
: 10
-10-006-852-2 (1-502) x US-09-938-842A-1810 (1-1509)

1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
1 ATGGTGCTCTCCACGCGCTATCGAGTTCGAGCTCGCTCCCTCCACTCCACATTCGATCA 60
21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
61 CGTTAGCTCCGACTTCACTTCTAGTTCAAGATGCCGGAATCCGATTCCTTAGGAA 120
41 AlaAlaTyrGlnIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
121 GCGGCGTATCAGATCATCAACGACGAGCTGATGCTTGACGGGAATCCACGGTTGAATTA 180
61 AlaSerPheValThrTrpMetGluProGluCysAspLysLeuIleValSerSerIle 80
181 GCCTCCTTTGTACGACATGATGAGCTGAGCTGATGATGATGATGATGATGATGATGAT 240
81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
241 AACAGAACTATGTTGACATGAGCGAGTACCCGCTCACCCGAACTTCAGAACCGATGT 300
101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
301 GTGAACATGATTGCACATCTATTCAATGACCCGTTAGAGAGCGGAGACCGCCGTCGGA 360
121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
361 GTAGGAACCGTTGGATCATCGAGGCGCATATGTTGGCCGTTTGGCCCTTCAAGCGTAAA 420
141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
421 TGGCAGAAACAGGCGAAAGCTGAGGCAAAACCCGTCGATAAACCCCACTTGTACCAGA 480
161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLysGlu 180
481 GCCATGTTCAAGTGTGGGAGAAATTCGTTAGGTACTTTGAGGTTGAACTTAAGGAA 540
181 ValLysLeuSerGluGlyTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
541 GTGAATGTAGTGAAGGATACTATGATGAGGACCCCTCAACAGCTGTTGATATGGTTGAT 600
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
601 GAGAACACCAATTTGTGTGGGCCATCTTGTTCCTCACTTTAATGGAGAATTCGAAGAT 660
221 ValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
661 GTTAAACTCTTGAACGATCTCTTGTGGTGAAGAGATCAATGTGAGTGGTCAAGATGGACTT 720
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
721 ATCCAGTGTGATCGGCAAGTGGAGATTCATTGACCGGTTTGTATCCGGAATTTGGA 780
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
781 TGGGACTTTAGACTTCCTCTGGTGAAGAGATCAATGTGAGTGGTCAAGATGGACTT 840
281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300
841 GTGTACCGAGGATTTGGTGTGGGTATCTGGAGAAACAAAGAGATTTGCTTGAGGAATC 900
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
901 ATCTTCCATATCAATTAATCTTGGTGTGACCAACCCACTTTACTCTCAATTTCTCCAA 960
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
961 GGTTCAAGTCAAGTCATTGCTCAATACCTACCACTATCCGATTTGGCCACGAGGGTTAC 1020
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QY 341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValValLeuArgGluGlyLeuGluLys 360
Db 1021 AGAAATGTGATGAGAAATTCAGAGAGAAATATGATCGTCTTAAGGGAAGACTTGAAG 1080
QY 361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
Db 1081 ACAGAAAGGTTCAACATCGTCTCAAGGAGCGAGGAGTGCACCTTGTCTTCTCTCTTG 1140
QY 381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgTyrGlyTyr 400
Db 1141 AAAGATGACGAGCTGCACACTGAGTTTGGAAATCTCCGACATGCTTCGAGGTATGATGG 1200
QY 401 IleValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgValVal 420
Db 1201 ATAGTGGCGCTACCAATCGCTCCAAATGCAACACATCACTGTTCTTCTGTGGTT 1260
QY 421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
Db 1261 ATCAGAGAAATTTCTGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
QY 441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
Db 1321 ATCGGTGAGCTCGATGAGTTCCTTCGAGAGTGAATTCACAAATATCACTTGGACAAGAG 1380
QY 461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
Db 1381 AAGAGTGAATCTAACACGATACTTGTATGCTCAGCGTGAAGAGCGGATATCGACAAG 1440
QY 481 GlnArgAspIleIleThrGlyTyrLysLysPheValAlaAspArgLysLysThrSerGly 500
Db 1441 CAGAGAGATATCATCACTGCTGGAAGAACTTTGTCCCGCAGAGAGACGAGTGGT 1500
QY 501 IleCys 502
Db 1501 ATCTGC 1506

RESULT 3
US-10-006-852-15
; Sequence 15, Application US/10006852
; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kinnerseley, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Petunia x hybrida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (72)..(1571)
; OTHER INFORMATION:
US-10-006-852-15

Alignment Scores:
Pred. No.: 4,19e-252 Length: 1785
Score: 2250.00 Matches: 427
Percent Similarity: 92.64% Conservative: 39
Best Local Similarity: 84.89% Mismatches: 33
Query Match: 86.04% Indels: 4
DB: 14 Gaps: 2

US-10-006-852-2 (1-502) x US-10-006-852-15 (1-1785)
QY 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
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72 ATGGTTCTATCAAGACAGTGTGCGAGAGCGATGTGTCCATTCACTCCACGTTTGCTTCT 131
21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
132 CGATATGTTCCGAACCTTCTCTCCAGGTTTAAATGCGAGATAATTCGATCCAAAGAA 191
41 AlaAlaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
192 GCAGCATATCAGATCAATAATGATGAATGATGTTAGATGGAAACCCCAAGGCTGAACCTG 251
61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
252 GCTTCTTTTGTACACATCGATGGATGGAAACCCAGAGTGTGATAAGTATGATGATGACTCTATT 311
81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
312 AACAAGACATATGTTGATATGGATGAATATCTGTACCACCTGACCTTCAGATCGATGT 371
101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
372 GTAAACATGATAGCTCATTTGTTTAAATGACCACTTGAAGATGGAGAACTGCAGTTGGA 431
121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
432 GTTGGAACTGTGGATCCTCTGAAGCCATATGCTTGTGGATTAGCTTTCAAGAGAAA 491
141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
492 TGGCAGACAAATAATGAAGCCCAAGCAACCTGTGACCAAGCCCAACATTTGTTACTGGT 551
161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
552 GCAAAATGTCCAGTGTGCTGGGAGAAATTTGCAAGGTATTTTGAAGTGGAGCTAAAGAA 611
181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnAlaValAspMetValAsp 200
612 GTAAAGCTTAGTGAAGATACTATGTATGTGACCTTGAGAAAGCTGTGAGATGTGGAT 671
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
672 GAAACACACATTTGTGTAGTGTCTTCTTAGTGTCCACCTCAATGGAGAAATTTGAAGAC 731
221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
732 GTTAAGCGCTTGAATGATCTCTTGTGGAGAGAACAAAGAAACCGGGGGGACACTCCA 791
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
792 ATTCAATGTGGATGCAGCAAGTGTGGATTTATTGACCGCTTCATTTACCCAGAGCTTGAG 851
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
852 TGGGACTTTAGATTGCAATTTAGTGAAGACATTAATGTAAAGTGGTCACAAATATGGTCTT 911
281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeu 300
912 GTCTATGCTGGTATGGTGTGGTGTGGAGAACCAAGATGATTTGCTCGATGACTT 971
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
972 ATCTTCCACATTAATATCTTGTGTGCTGATCAACCTACTTCACTCTCAACTTTTCTAAA 1031
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
1032 GGTTCTAGCAAGTAATGTCTCAATATTTACCACTTATTCCGCTTGGGTTATGAGGGTTAC 1091
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
1092 AAGAATGTGATGGAGATTTCTCAAGAAATTCATCGTACTAAGAGAGGGCTAGAAAG 1151
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
1152 ACAGGAAGATTCAACATAATCTCCAAAGAAATTTGGAGTACCTTTTAGTAGCTTCTCTCT 1211

381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTrp 400
1212 AAAGACAACAGGCAACACACAGAGTTCGAGATTTCTGAAACTTTAAGGAGATTTGGTTGG 1271
401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
1272 ATTGTTCTCTGCATATATCTATGCCCAACGCAACACATTTACAGTTCTCAGAGTTGTG 1331
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
1332 ATCAGAGAAAGATTTCTCCGTACGTTGCAAGACGACTGTGTAAAGACATCGAAAAAGTC 1391
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
1392 CTTTCATGAACCTTGACACACTCCCTGCGCTGCAATGTCTAAGCTCGCTGGCCGAGGAG 1451
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1452 CAGCGCGCTGCGAATGGCAGCGAGGTGCAT-----AAGAAAACAGATAGCGAAGTG 1502
481 GlnArgAspIleIleThrGlyTrpLysLysPheValAlaAsp---ArgLysLysThrSer 499
1503 CAGTTCGAGATGATACTGCATGGAGAAAGTTTGTGAAGAAAAGAGAGAGACTAAT 1562
500 GlyIleCys 502
1563 CGAGTTTGT 1571

RESULT 4
US-10-006-852-11
; Sequence 11, Application US/10006852
; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kinnersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1705
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (71)..(1558)
; OTHER INFORMATION:
US-10-006-852-11

Alignment Scores:
Pred. No.: 5,72e-251 Length: 1705
Score: 2240.00 Matches: 428
Percent Similarity: 92.05% Conservative: 35
Best Local Similarity: 85.09% Mismatches: 32
Query Match: 85.66% Indels: 8
DB: 14 Gaps: 3

US-10-006-852-2 (1-502) x US-10-006-852-11 (1-1705)

Qy 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 71 ATGGTTCTGTCCAAAGCAGCGTCGGAAGTGCAGTCTCCACTCCACTTTCGCTTCC 130
Qy 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
Db 131 CGATATGTTCTGACTTCTCTCCAGGTTTAAAGTGCAGAAATTCGATACCAAGAA 190
Qy 41 AlaAlaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60


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191 GCAGCATATCAAAATCAATAATGATGAGCTTATGTTAGATGGAATCCAAAGACTAAATTTA 250
/
61 AlaSerPheValThrTrpMetGluProGluCysAspLysLeuIleMetSerIle 80
>
251 GCATCTTTGTGCAACATGGATGGAAACGAGGTGAACAAACTGATGATGGATTCCTT 310
/
81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
>
311 AACAAAGAAATTCAGTTGATGGATGAATACCCCTGTTAACCACTGAACCTTCAGAAATCGATGT 370
/
101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
>
371 GTAACATGATAGTACTCATTTGTTTAAACGACCACTTGGAGATGGAGAGACTCGAGTTGGA 430
/
121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
>
431 GTTGGAACTGTTGATCCTCTGAGGCTATTATGCTTGCTGGATTAGCTTTCAGAGAGAAA 490
/
141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
>
491 TGGCAAAATAAAATGAAGCCCAAGCAAGCCCTGTGACAAGCCCAATATTGTCACTGGT 550
/
161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
>
551 GCCNATGTCAGGTGTGTTGGGAGAAATTTGCAAGGTATTTTGAAGTGAGACTAAAGGAA 610
/
181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
b
611 GTAAAGTTGATGTGATGATACTATGTGATGACCCCTGAGAAAGCTGTGAAATGTTGGAT 670
/
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLysAsnGlyGluPheGluAsp 220
b
671 GAGAACAAATTTGTGTAGTGTCTATCTTGGGTTCACACTCAATGGTGAATTTGAAGAT 730
/
221 ValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240
b
731 GTTAAGGCTTGTATGACCTCTTGATGTGAGAAGAACAAAGAACCCGGTGGACACTCCA 790
/
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
b
791 ATTCATGTGGATGAGCAAGTGGTGGATTTATTGCACCATTCCTTTATCCAGAGCTTGAA 850
/
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
b
851 TGGACATTTAGATTGCATTTGGTGAAGAGTAAACGTGAGTGGTCACAAATATGTCCT 910
/
281 ValTyrAlaGlyIleGlyTyrPheIleTyrArgAsnLysGluAspLeuProGluGluLeu 300
b
911 GTTTATGCTGTTATGTTGGGCCATTTGGAGGAATAAGGAAGACTTACCTGCAGCACTT 970
/
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
b
971 ATCTTCCACATTAATATATCTGTGGTGTGATCAACCTACTTCACTCTCAACTTCTCTAA 1030
/
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
b
1031 GGTCTAGCAAGTAATGCTCAATATTACCACTTATTCGCTTGGGTTTTGAGGGTTAC 1090
/
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
b
1091 AAGAATGTTATGGAGAATTTGCAAGAAAATGCAAGGCTACTAAGAGAAGACTTGA AAAA 1150
>
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
>
1151 AGTGGAGATTCACATPAATTCGAAGAAATTTGGAGTTCCATTAGTGTCTCTCTCT 1210
/
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgTyrGlyTyr 400
>
1211 AAAGACAACAGTCAACACAAATGAGTTGCAAAATTTCTGAAACTCTTAGAAGATTTGGATGG 1270
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401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
>
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Db 1271 ATTATTCCTGCATATACTATGCCACCAAAATGCTCAACATGTCACAGTTCTCAGAGTTGTC 1330
Qy 421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
Db 1331 ATTAGAAAGATTTCTCCGTACACTCCGCGAGCTGTAATAGACATTTGAAAAGTTC 1390
Qy 441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
Db 1391 CTCACAGAGCTAGACACACTTCGCGCGAGGGTCAACGCTAAGCTAGCCGTG----- 1441
Qy 461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
Db 1442 ---GCCAGGCGGAATGGCAGCGGTGCAT-----AAGAAAACAGATAGAGAGTG 1489
Qy 481 GlnArgAspIleIleThrGlyTyrLysLysPheValAlaAsp---ArgLysLysThrSer 499
Db 1490 CAGCTTGAGATTACTACTGTCATGGAAGAAATTTGTTGCTGATAGAGAGAGAGACTAAC 1549
Qy 500 GlyIleCys 502
Db 1550 GGAGTTTGT 1558

RESULT 5
US-10-005-602-1
; Sequence 1, Application US/10005602
; Publication No. US20030110530A1
; GENERAL INFORMATION:
; APPLICANT: Barry Shelp
; APPLICANT: Alan Bown
; TITLE OF INVENTION: TRANSGENIC PLANTS HAVING REDUCED
; TITLE OF INVENTION: SUSCEPTIBILITY TO INVERTEBRATE PESTS
; FILE REFERENCE: P84US3
; CURRENT APPLICATION NUMBER: US/10/005,602
; CURRENT FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1745
; TYPE: DNA
; ORGANISM: tobacco plant
US-10-005-602-1

Alignment Scores:
Pred. No.: 3,89e-250 Length: 1745
Score: 2233.00 Matches: 427
Percent Similarity: 91.85% Conservative: 35
Best Local Similarity: 84.89% Mismatches: 33
Query Match: 85.39% Indels: 8
DB: 14 Gaps: 3

US-10-006-852-2 (1-502) x US-10-005-602-1 (1-1745)
Qy 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 31 ATGTTCTGCTCCAAAGACAGCGTGGAAAGTGCAGCTTCTCCATCCACTCCACTTCGCTTCC 90
Qy 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
Db 91 CGATATGTTCCGAACCTTCTCTCCAGGTTTAAAGATGCCAGAGAAATTCATATCCAAAGGAA 150
Qy 41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
Db 151 GCAGCATATCAGATTATAAATGATGAGCTTATGTTAGATGGAAATCCAAAGGCTAAATTTA 210
Qy 61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
Db 211 GCATCTTTTCGTTTCAACATGGATGGAGCCAGAAATGAATACGTTAATGATGGATTCAT 270
Qy 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
Db 271 AACAGAACTACGTTGACATGGATGATACCTCTGAACCACTGAGCTTCAGAAATCGATGT 330
Qy 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
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331 GTAAATATGATAGCTCATTTGTTTAAATGACCACTTGGAGATGGAGACTCGACTTGA 390
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121 ValGlyThrValGlySerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
|||||
391 GTTGGAACTGTTGGATCCTCTGAGACTATATGCTTGCTGGATTAGCCTTTAAAGAAAA 450
|||||
141 TrpGlnAsnLysArgLysAlaGlyLysProValAspLysProAsnIleValThrGly 160
|||||
451 TGGCAAAATAAATGAAGCCCAAGGAGCCCTTTGATAAGCCCAATATCGTCACCGGT 510
|||||
161 AlaAsnValGlnValCysTrpGluLysPheAlaAaGlyTyrPheGluValGlnLysGlu 180
|||||
511 GCTAAATGTCAGGTGTTGGGAGAAATTTGCAAGGTAATTTTGAAGTGGAGTTGAAGAA 570
|||||
181 ValLysLeuSerGluGlyTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
|||||
571 GTPAAATTTGAGTGATGATACATATGATGGACCTTGAGAAAGCTGTGGAATGGTGGAT 630
|||||
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
|||||
631 GAGAAATACCAATTTGCTGTCTATCTTAGGTTCAACACTCAATGGTCAATTTGAAAGT 690
|||||
221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
|||||
691 GTTAAAGCTTTGAATGACCTTTTGATTTGAGAGAACAAAGAACCCGGTGGGACACTCA 750
|||||
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
|||||
751 ATTATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 810
|||||
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
|||||
811 TGGGACTTTAGATGTCATTTGGTGAAGAGATTAATGTGAGTGGTCAACAAATATGGTCT 870
|||||
281 ValTyrAlaGlyIleGlyTyrValIleTyrAsnLysGluAspLeuProGluLeuLeu 300
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871 GTCATATGCTGATATGTTGGGCCATTTGGAGGAATPAGGAAGACTTGGCTGATGAAC 930
|||||
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
|||||
931 ATTTTCCACATCAATTACCTTGGTGTGATCAACCTTACTTCACTCTCAACTTCTCTAAA 990
|||||
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
|||||
991 GGTCTAGCCCAAGTAATGCTCAATATATACCAACTTATTGCTTGGGTTTGGAGGTTAC 1050
|||||
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
|||||
1051 AAGAATGTTATGAGGAATTTGTCAGGAATATGCAAGGTTATTAAGAGAAGAAATGNAAAA 1110
|||||
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
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1111 AGTGAAGATTCAACATAATCTCCAAAGAAATTTGGAGTTCCCTTAGTCAATTTCTCTTT 1170
|||||
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr 400
|||||
1171 AAGACAAACAGTCAACACAATGATGTTGAAATTTCTGAAGATTTGGATGG 1230
|||||
401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
|||||
1231 ATTGTTCTTCATATATATATGCCCACCAATGCTCAACATGTTACATTTCTCAGAGTTGTC 1290
|||||
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
|||||
1291 ATTAGAAGATTTCTCCCGCACACTAGCCGAGCGACTGTAATAGACATTTGAAAAAGTC 1350
|||||
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
|||||
1351 CTCACAGCTAGACACACTTCGCGGAGGGTCAACGCTAAGCTAGCCGTG----- 1401
|||||
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
|||||
```

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121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
122 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
361 GTGGGACGGTGGGTTCTGTCGAGGCGCATCATGCTGGCGGGCTGGCCCTTCAAGCGGGC 420
141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
142 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
421 TGGCAGAAACAAGCGCAAGCGCGGAGGAGCGGTTCCGACAAGCCCAACATCATCACCGGC 480
161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
162 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
481 GCCAAGTGCAGGTGTCTGGGAGAGTTCCGCCGCTACTTCGAGGTGAGCTCAAGGAG 540
181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
182 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
541 GTGAAGCTCCGCGAGCTACTACGTATCATGGACCCCGAGAAGCCGTCACATGTGTCAAC 600
201 GluAsnThrIleCysValAlaAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
202 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
601 GAGAACACCATCTGCGTGGCGCCATCTCGGCTCCACCCTCAACGCGGAGTTCGAGGAC 660
221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
222 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
661 GTCAAAGTCTCAACGACCTCTCTCGACAAGAGAACAGAGACTGGGTGGGAGAGCGCG 720
241 IleHisValAspAlaIleAspGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
721 ATCCAGTGTGACGCGGAGCGCGGGTTCATCGCGCGTTCCTGTACCGGAGCTGGAG 780
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
781 TGGGACTTCGGGTGCGGTGGGTGAAGAGCATCAAGTGAAGCGGTCAAGTACGGGCTC 840
281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeu 300
841 GTCTACGCGGCATCGCTGGTGCATCTCGCGCAACAAGAGGACCTGCCCGAGGAGCTC 900
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
901 ATCTTCACATCAACTACCTCGGCGCGGACCGACCAACCTTCAACCTTCACTTCCCAAG 960
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
961 GGTCTCCAGCGAGTATCGGCCGAGTACTACAGCTCATCGCCACCGGCTTCGAGGGGTAC 1020
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
1021 AGGAACATCATGAGAACTGCCACGAGAACCGCATGGTGTGAAGGAAGGGCTGGTGAAG 1080
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
1081 ACGGGAGGTTCGACATCGTGTCCAGGAGCAAGGGGTGCGGTGGTGGCTTCGCTC 1140
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr 400
1141 AAGGACCGGAGCGGACGACGAGTTCGAGATCTCCGACATGCTGCGCGCTTCGCTGG 1200
401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
1201 ATCGTGGCGGTAACCATATGCGCGCGCGACGCGCACGATCGCTGCTGGTGGTGGTGC 1260
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
1261 ATCGGAGGAGGTTCACCGCACCTCGCGAGCGCTCGCTCGACATCGAAGAGGTG 1320
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
1321 ATGTACCAAGCTCGACGCGCTCCCTCCAGGCTCATGCCCGCGCGCGCGCGCGCGCG 1377
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1378 -----CTGCTGGTGGTCCCAAGAGTCCGAGCTCGAGACG 1413
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Oy 481 GlnArgAspIleIleThrGlyTrpLysPheValAlaAspArgLysLysThrSerGly 500
Db 1414 CAGCGTGGTGCAGGAGGCGTGGAGAGTTCGTGTCTC---GCCAAGAGGACCAACGCGC 1470
Oy 501 IleCys 502
Db 1471 GTCGTC 1476

RESULT 7
US-10-006-852-13
; Sequence 13, Application US/10006852
; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kinnersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 1771
; TYPE: DNA
; ORGANISM: Nicotiana tabacum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (67)..(1554)
; OTHER INFORMATION:
US-10-006-852-13

Alignment Scores:
Pred. No.: 3,7e-246 Length: 1771
Score: 2199.00 Matches: 423
Percent Similarity: 90.85% Conservative: 34
Best Local Similarity: 84.10% Mismatches: 38
Query Match: 84.09% Indels: 8
DB: 14 Gaps: 3

US-10-006-852-2 (1-502) x US-10-006-852-13 (1-1771)
Oy 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 67 ATGGTTCGTCCAAAGACAGCGTCGAAAGTACGCTCCGFTCACTCCACTCCACTTCGCCTCC 126
Oy 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
Db 127 CGATATGTTCCAACTTCTCTCCAGGTTTAAATGCCAGAGAATTCAATACCAAGGAA 186
Oy 41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
Db 187 GCAGCATATCAGATTATAAATGATGAGCTTATGTATGATGAAATCCAAAGCTAAATTTA 246
Oy 61 AlaSerPheValThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
Db 247 GCACTTTCGTTACACATGATGAGTGGAGCCAGAAATGTAATACGTTAATGATGGATTCCATT 306
Oy 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
Db 307 AACAAAGAACTACGTTGATGATGATATACCTGTAAACCACTGAGCTTCAGATCGATGT 366
Oy 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGly 120
Db 367 GTAAATATGATAGCTCATTTTGTAAATGCACCACTTGGAGATGGAGAGCTGCAAGTTGGA 426
Oy 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
Db 427 GTTGAAGTGTGGATCCTCTGAAGCTATTATGTTGCTGGATTAGCTTTAAGAGAAA 486
Oy 141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
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487 TGGCAAAATAAAATGAAGCCCAAGCAAGCCCTTTGATAAGCCCAATAATTGTCAACCGT 546
161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
547 GCTAATGTCAGGTGTCTGGGAGAAATTTGACAGTATTTTGAAGTGGAGTTGAAGAA 606
181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
607 GTAAAAATTGAGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 666
201 GluAsnThrIleCysValAlaAlaPheLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
667 GAGAAATACCATTTGTGTGCTACTTCTAGGTTCACACACTCAATGGTGAATTTGAAGAT 726
221 ValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240
727 GTTAAGCGTTTGAATGACCTTTTGAATGAGAGAACAAAGAACCGGTGGACACTCCA 786
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
787 ATTCAATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 846
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
847 TGGGACTTTAGATTGCAATTTGGAGAGAGATTAATGTGAGTGGTCCACAAATATGCTCT 906
281 ValTyrAlaGlyIleGlyTyrValIleTyrArgAsnLysGluAspLeuProGluLeu 300
907 GTCTATGCTGTTATGTTGGGCCATTTGGAGGAATAAGGAAGACTTGCCTGATGAACCT 966
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
967 ATTTTCCACATCAATACCTTGTGTGTGATGATGATGATGATGATGATGATGATGAT 1026
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
1027 GGTTCAGCAAGTAATTTGCTCAATTAATACCACTTAATTCGCTTGGGTTTGGAGGTTAC 1086
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuLys 360
1087 AAGAATGTTATGAGAAATTTGCAAGAAATGCAAGGTTATTAAGAGAGAAATTAAGAAA 1146
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
1147 AGTGGAGATTTCAACATAATTCCTCAAGAAATTTGGAGTTCCCTTAGTAGCATTTCTCT 1206
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgTyrGlyTyr 400
1207 AAGACACACAGTCAACACATGAGTTTCAAAATTTCTGAACCTTTAGAGAGATTGGATGG 1266
401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
1267 ATTGTTCTGTCATATACTATGCCACCAATGCTCAACATGTCACAGTTCTCAGAGTTGTC 1326
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
1327 ATTAGAGAGATTTCTCCCGCACACATAGCGAGCGACTGTGTAATAGACATTGAAAAGTC 1386
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
1387 TTCACCGAGTAGACACACTTCCGCGAGGGTCAACGCTAAGCTAGCCGTG----- 1437
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1438 ---GCCAGGCGAATGCGCGCGTGCAT-----AAGAAAAACAGATAGAGAAGTG 1485
481 GlnArgAspIleIleThrGlyTyrLysLysPheValAlaAsp---ArgLysLysThrSer 499
1486 CAGCTAGAGATTACTACTGCTGATGTTGAAATTTGTTGCTGATTAAGAGAGAAAGACTAAT 1545
500 GlyIleCys 502
1546 GGAGTTTGT 1554

RESULT 8

US-09-938-842A-937
; Sequence 937, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 937
; LENGTH: 1482
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-937

Alignment Scores:
Pred. No.: 7,22e-239 Length: 1482
Score: 2135.50 Matches: 411
Percent Similarity: 88.78% Conservatives: 32
Best Local Similarity: 82.36% Mismatches: 45
Query Match: 81.66% Indels: 11
DB: 10 Gaps: 2

US-10-006-852-2 (1-502) x US-09-938-842A-937 (1-1482)

Qy 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 1 ATGGTTTGTCTAAGACAGATTTCGGAATCTGATCTCAATCCATTCATCTTTTGTCTCT 60
Qy 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
Db 61 CGTTACGTCGCGCAACTCTCTTCCACGATTGAAATGCTCGAGAACTCAATCCCAAGAA 120
Qy 41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
Db 121 GCAGCTTACCAATATCATCAGCAGAGCTAATGCTCGATGGTAACCCAGGCTGAACCTA 180
Qy 61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
Db 181 GCTTCTCTCGTGACCATGATGGAGCCAGAAATGTGCAAGCTCATGATGGAGTCCATC 240
Qy 81 AsnLysAsnTyrValAspMetAspGlyTyrProValThrGluLeuGlnAsnArgCys 100
Db 241 AACAGAACTACGTCGACATGAGCAGAGTACCCTGTCCACTGAGCTTCAGAACCGATGT 300
Qy 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGly 120
Db 301 GTTAACATGATAGCACGCTCTCTTCAACGCGCGCTTGGTGACGGTGAAGCTGCGTTGGT 360
Qy 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
Db 361 GTTGGCACCGTCGGATCGTCGAGCGCATATATGTGTGGCCGCTTTGGCTTTTAAGAGCAA 420
Qy 141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
Db 421 TGGCAGAAATAAGCTGAGGCCCAAGGGCTTCTCTTATGATAGCCCAATATCGTAACCGGT 480
Qy 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
Db 481 GCTAATGTCCAGGTTTGTCTGGAGAAATTCGCAAGGTTATTTGGAAGTGGAGCTTAAGGAA 540

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181 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
182 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
183 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
541 GTGAACCTTAAGAGAGACTATTACGTGATGGACCTGTAAGAGCGGTGAAATGCTAGAC 600
542 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
202 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
601 GAAACACAAATTGTCTGCTGCTCCATCTCTCGGTTCACACGTTAAACCGGTGAATTCGAAGAC 660
602 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
221 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
661 GTTAAGCTCTCAACGACCTCTCTGTGAGAAAACAAGCAACCGGATGGACACGCA 720
721 ValLysLeuSerGluGlyTyrThrValMetAspProGlnAlaValAspMetValAsp 200
241 IleHisValAspAlaAspSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
721 ATACAGCTGGACGACGAGTGTGGGTTTATTGCTCCGTTCTGTATCCGAGCTGGAG 780
781 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisGlyTyrGlyLeu 280
781 TGGGATTTCCGGCTACCGTTGGTTAGAGATTAATGTAGTGGGTCAACAAATACGGTTTG 840
281 ValTyrAlaGlyIleGlyTyrValIleTyrPheAsnLysGluAspLeuProGluLeu 300
841 GTTACGCGCGGTATTGGTTGGTTGTATGGAGAACCAACCGGATTCGCTGATGAATT 900
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
901 ATCTTCATATCAATTAATCTTGGCGCTGATCAACCAACCTTTACACTCAACTTCCTCAA 960
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
961 GGTTCAAGTCAAGTGAATGCTCAGTACTACCGCTGATTCGCTGTTGGATTCGAGGTTAT 1020
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlyLys 360
1021 CGCAATGTATGATGATTAATGTTCGGGAAACATGATGCTACTAAGCAACAGGATTAGAAA 1080
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
1081 ACGGGACGTTTTAAAAATCGCTCTCAAGAAAACCGGTGTTCCGTTAGTGGCGTTTTCTCTC 1140
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr 400
1141 AAGATAGTAGCCGCCACACGAGTTCGAGGTGGCCCATACCTCGCTCGCTTCGCTGG 1200
401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
1201 ATCGTTCCGCGCTACAGATGCTCGGATGCGCAGCATGTCACTGCTTCGAGTTGTT 1260
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGlyLysVal 440
1261 ATCCGAGAAGATTCTCTCAACCTTTAGCCGAGAGATTGGTACTGATTTCCGAGAGGTT 1320
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
1321 CTACAGAGCTCGATACGCTTCGCGGAGGTTTCAGCCAGATGCTATGGAAAAGTT 1380
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1381 AACGGT-----GTTAAGAAGACGCCAGAGGAGACG 1410
481 GluArgAspIleIleThrGlyTyrLysPheValAlaAspArgLysIleThrSer 499
1411 CAGAGAAGATCAGCGCTACTCGAAGAGTTTGTG---GAGACTAAGAAGACCAAC 1464

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RESULT 9

US-10-006-852-3

Sequence 3, Application US/10006852

Publication No. US20030046732A1

GENERAL INFORMATION:

APPLICANT: Kinnersely, Alan M.

APPLICANT: Turano, Frank J.

TITLE OF INVENTION: Methods for Regulating Plant GABA Production

```

; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (17)..(1498)
; OTHER INFORMATION:
US-10-006-852-3

Alignment Scores:
  Length: 1665
  Score: 2130.00
  Percent Similarity: 89.29%
  Best Local Similarity: 80.16%
  Query Match: 81.45%
  DB: 14
  Gaps: 3

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US-10-006-852-2 (1-502) x US-10-006-852-3 (1-1665)

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Qy 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 17 ATGTTTGGACAAAACCGCAACG--AATGATGAATCTGCTGCACCATGTTCCGGATCT 73
Qy 21 ArgTyrValArgThrSerLeuProArgPheLysMetProLysSerIleProLysGlu 40
Db 74 CGCTATGTTGCGACTACACTTCCCAAGTATGAGATTCGTGAGATTCGATACCGAAGAC 133
Qy 41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
Db 134 GCTGCATATCAGATCATAAAGATGAGCTGATGCTGATGTTAACCCGAGGCTTAACCTA 193
Qy 61 AlaSerPheValThrTyrMetGluProGluCysAspLysIleMetSerSerIle 80
Db 194 GCTTCGTTTGTGACTACATGATGGAACGAGAGTGTGACAACTCATATGAGACTCTATC 253
Qy 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
Db 254 AACAGAACTACGTTGATGATGAGTACCTGCTCAACTGAGCTCCAGAACCGATGT 313
Qy 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGly 120
Db 314 GTAAACATTATAGCTCCGACTGTTCAATGCCCATCTCGAGGATCTGAGACGGCGTGGGA 373
Qy 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
Db 374 GTAGGACAGTGTGTTCTTTCAGAAAGCCATCATGTTAGCCGATTTGGCTTCAAAAGAAA 433
Qy 141 TrpGlnAsnLysArgLysAlaGluGlySerProValAspLysProAsnIleValThrGly 160
Db 434 TGGCAGAAACAACCGCAGGCTGAGGCTAAACCCCTATGCAACCCCAACATTTGTCACCTGA 493
Qy 161 AlaAsnValGlnValCysTyrLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
Db 494 GCCAATGTTCAAGTTTGTGGGAGAAATTCGCTCGGTACTTTCGAGGTGGAGCTAAAGGAA 553
Qy 181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
Db 554 GTAAACCTTAAGTGAAGGTTACTACGTGATGATGATCCAGAACGAGCAGAAATGCTAGAC 613
Qy 201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrIleAsnGlyGluPheGluAsp 220
Db 614 GAGAACACAATCTGTGTCGAGCCATATTTGGGATTCACACTCAACCGGTGAGTTCCGAGAC 673
Qy 221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240

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674 GTGAACCGTCTCAATGACTTGCTAGTCAAGAAAAACGAGGAGACTGGTTGGAACACACCG 733
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
734 ATCCACGTGGATGACAGCAAGTGGAGGGTTCAAGTCCGTTTATCTATCTGTAATTAGAA 793
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
794 TGGGACTTTAGACTTCCTTTGGTTAAGATATCAACGTGAGTGGTCAACAAGTATGCACTG 853
281 ValTyrAlaGlyIleGlyTyrValIleTyrArgAsnLysGluAspLeuProGluLeu 300
854 GTCATGCTGGTATGTTGGTTGGTGGTGGAGGGCAGCAGAGATTGCTCAAGAGCTT 913
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
914 ATCTTTCAATTAATATCTTGGTGTGATCAACCCACTTTCACCTCAATTTCTCCAG 973
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
974 GGATCGAGCCAAATATTGCTCAATACTACCAAGCTCATTCGCTTGGATTCCAGGGGTAC 1033
341 ArgAsnValMetClnAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuLys 360
1034 AAAAATGTTGATGGAGAAATTCATAGAGAACATGGTGGTTCTCAAGAGAGGATAGAGAA 1093
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
1094 ACAGAGGGTTTCAACATAGTCTCAAGAGCAACAGGAGTCCAGTCTGATGCCCTTCTCTC 1153
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgTyrGlyTyr 400
1154 AAGGACCATAGTTTCCACAAACGAGTTCGAGATCTCTGAGATGCTACGTCTGTTGGCTGG 1213
401 IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal 420
1214 ATCGTCCAGCTTACACTATGCTCCGCGATGCACACATCATCGGTTCTGGTGTGTC 1273
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
1274 ATCAGGGAAGATTTCACAGAACACCTCGCGGAGAGACTTGTGCTGATATTTCGAAGGTG 1333
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlnGlu 460
1334 CTTTCATGAGCTAGATACCTTGGCTTCCAAAGATATCTAAGAAGATGGGAATA----- 1384
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1385 -----GAAGGGATCGCGGAAAAATGTAAGGAGAGAGAGATGGAGAG 1426
481 Gln-----ArgAspIleIleThrGlyTyrLysLysPheValAlaAspArgLysThr 498
1427 GAGATCTGATGGAAGTATTGTTGGATGGAGGAAGTTTGTGAAGGAGAGAGAGATG 1486
499 SerGlyIleCys 502
1487 AATGGGTGTGTGC 1498
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RESULT 10

S-10-167-547C-1

Sequence 1, Application US/10167547C

Publication No. US20030170653A1

GENERAL INFORMATION:

APPLICANT: E.I. du Pont de Nemours and Company

APPLICANT: Damude, Howard G.

TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma

TITLE OF INVENTION: Butyrolactone and its intermediates

FILE REFERENCE: CIL804 US NA

CURRENT APPLICATION NUMBER: US/10/167,547C

PRIOR FILING DATE: 2003-03-17

PRIOR FILING DATE: 2001-06-08

NUMBER OF SEQ ID NOS: 67

; SOFTWARE: Microsoft Office 07

; SEQ ID NO 1

; LENGTH: 1497

; TYPE: DNA

; ORGANISM: Alstroemeria

US-10-167-547C-1

Alignment Scores:

Pred. No.:	1,44e-231	Length:	1497
Score:	2073.00	Matches:	391
Percent Similarity:	87.92%	Conservative:	53
Best Local Similarity:	77.43%	Mismatches:	51
Query Match:	79.27%	Indels:	10
DB:	12	Gaps:	2

US-10-006-852-2 (1-502) x US-10-167-547C-1 (1-1497)

QY	1	MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer	20
DB	1	ATGTTTCTCTCCAGCGCGTCTCGACACACACCGGCCAGTCCACTGCACCTTCGCGTGG	60
QY	21	ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu	40
DB	61	CGTTACGTCCGCGATGCGCTGCCGCTTCAGGATGCCGAGATTTCGATACCCAGGAC	120
QY	41	AlaAlaTyrGlnIleIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu	60
DB	121	ACGCGGTACAGATCGTCAACGACGAGCTGATGCTGGACGCGAACCCAGGCTGAACCTG	180
QY	61	AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle	80
DB	181	CGTCGTTGTCACGACTGATGGAGCCGAGTGGATCGCTCATGATCGCGCGGCC	240
QY	81	AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys	100
DB	241	AACAAGAACTATGTCGACATCGGACGAGTACCCGCTCAACAACCGAGCTACAGAATCGCTGT	300
QY	101	ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly	120
DB	301	GTTAATATAATAGCCCACTCTTCAATGCGCTATTGGGGATGAGGAAACAGCAGTAGGA	360
QY	121	ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys	140
DB	361	GTTGGGACAGTGGGGTTCATCAGAACCAATATGCTTCAGCTTGGCTTCAGAGAAAG	420
QY	141	TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly	160
DB	421	TGGCAGAACCAAAAAAAGCAGAGGGGAAGCCATATGACAAGCCCAATATTGTCAACCGT	480
QY	161	AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu	180
DB	481	GCAACCGTTCAGGTTGCTGGGAAATTCGCTAGGTATTGTAAGTTGAACTGAAAGAA	540
QY	181	ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp	200
DB	541	GTGAAGCTGAGGGAGGGTTATTACATCATGGACCCAGAGAGGCTGTGGAAATGGTGGAT	600
QY	201	GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp	220
DB	601	GAGAATACCATATGTGTGCTGCTATCTTGGGCTCAACCCCTTACTGGAGAGTTCGAAGAT	660
QY	221	ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro	240
DB	661	GTTAAACTACTGAAACAACTCTTTGAAGAGAGAAACAAGGAAACTGGGTGGGACACACCC	720
QY	241	IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu	260
DB	721	ATTCAATGTTGATGCTAGTGGTGGATTCTTCTCTTCTATACCCAGAACTGAA	780
QY	261	TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu	280
DB	781	TGGGATTTCCGATTACCACTGGTGAAGAGTATTAAATGTGCGGACACAAATATGGCCTT	840

320 LysGlySerSerGlnValIleAlaGlnTyrGlnLeuLeuIleArgLeuGlyHisGluGly 339
y
966 AAAGGTTCTCTATCAAATATGACAGTATTATCAGTTAATAAGACTTGGCTTTGAGGGT 1025
b
340 TyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlu 359
y
1026 TATAAGAACGTCATGAAGAATTGCTTTATCAACGCAAAAGTACTTAACAGAGGAATCA 1085
b
360 LysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSer 379
y
1086 AAAATGGGCGGTTTCATATGTTCTCTAAGGATCTGGGTCTTCTGTGATGATTTTCT 1145
b
380 LeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgTyrGly 399
y
1146 CTCAGGACAGCAGCAAAATATACGGTATTGGAATATCTCAGCATCTCAGAAGATTGGA 1205
b
400 TrpIleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgVal 419
y
1206 TGGATCGTCCCTGCATACAAATGCCCACCGGATGCTGAACACATTCCTGTACTCGGGT 1265
b
420 ValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLys 439
y
1266 GTCAATTAGAGAGGATTTCAGCCACAGCTAGCTGAGAGACTTGTTCACATTGAGAAA 1325
b
440 ValMetArgGluLeuAspGluLeuProSerArgValIleHisLysIle-----SerLeu 457
y
1326 ATTCTGTCAAGTTGGACACACAGCCTCTCGTTGCCCCAACAAAGCTCTCGTGTCACT 1385
b
458 GlyGlnGluLysSerGluSerAsnSerAspAsnLeu-----MetValThrVal 473
y
1386 GCTGAGAGAGTGGTATGACAAAGGTGATGGCTTCATCATTTTCACATGGATCTGTA 1445
b
474 LysLysSerAspIleAspLysGlnArgAspIleIleThrGlyTrpLysLysPheValAla 493
y
1446 -----GAGACTCAGAAAGACATTATCAAACTTTGGAGGAAATCGCAGGG 1490
b
494 AspArgLysLysThrSerGlyIleCys 502
y
1491 -----AAGAAGACCAAGCGAGTCTGC 1511
b

RESULT 12

S-09-887-576-782

Sequence 782, Application US/09887576

Patent No. US2002014047A1

GENERAL INFORMATION:

APPLICANT: Budworth, P.

APPLICANT: Brown, D.

APPLICANT: Chang, H.

APPLICANT: Zhu, T.

APPLICANT: Han, B.

APPLICANT: Wang, X.

APPLICANT: Cooper, Bret

TITLE OF INVENTION: Promoters for regulation of plant expression

FILE REFERENCE: 1360.001US1

CURRENT APPLICATION NUMBER: US/09/887,576

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/213,848

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/258,692

PRIOR FILING DATE: 2000-12-29

NUMBER OF SEQ ID NOS: 875

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 782

LENGTH: 1455

TYPE: DNA

ORGANISM: Oryza sativa

JS-09-887-576-782

Alignment Scores:

Pred. No.:

6.97e-224

Length:

1455

Score: 2007.00 Matches: 381
Percent Similarity: 87.67% Conservative: 60
Best Local Similarity: 75.75% Mismatches: 42
Query Match: 76.75% Indels: 20
Dbs: 10 Gaps: 6

US-10-006-852-2 (1-502) x US-09-887-576-782 (1-1455)

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Qy 20 SerArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLys 39
Db 55 TCGCGGTACGTGCGACGGCTCCCGAGGTTCAGGATGCCGAGAAATCGATCCCCAAG 114
Qy 40 GluAlaAlaTyrGlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsn 59
Db 115 GACGGGGGTACAGATCATCAACGACGAGCTGATGCTCGACGGCAACCCGCGCTGAAC 174
Qy 60 LeuAlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSer 79
Db 175 CTGGCGTCTTTCGTCAACACGTCGATGGAGCCGAGTCGACAAAGCTCATGTGCGGCC 234
Qy 80 IleAsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGluAsnArg 99
Db 235 ATCAACAAGAATCTAGTCGATGATGATGATGATGATGATGATGATGATGATGATGAT 294
Qy 100 CysValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaVal 119
Db 295 TGGCTGAACATGATCGCGCATCTGTTCAACGCGCGATCGGGGACGACGACGCGGCTC 354
Qy 120 GlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArg 139
Db 355 GGGGTGGGCACGGTGGGTGCTCGAGGCCATCATGCTGGCGGGCTGCGCTTCAAGAGG 414
Qy 140 LysTrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThr 159
Db 415 AAGTGGCAGAACAGGATGAAGCCGAGGGGGAAGCCCCACGACAGCCCAACATCTGTGAG 474
Qy 160 GlyAlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLys 179
Db 475 GGGGCCAAGTGCAGGTGCTGGGAGAGTTCGCGCGCTACTTCGAGGTGGAGTCAAG 534
Qy 180 GluValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetVal 199
Db 535 GAGGTGAAGCTGACCAAGGGTACTACGTGATGAACCCGAGAGAGCCGCGTGGAGTGTGC 594
Qy 200 AspGluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGlu 219
Db 595 GACGAGAACCATCTGGCTGCCGCCATCTCTCGGCTCCACCTCAACGGCGAGTTCGAG 654
Qy 220 AspValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThr 239
Db 655 GACGTCAAGATGCTCAACGACCTCTCCCGCAAGAACCGCGACAGAGGTGGAAACAG 714
Qy 240 ProIleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeu 259
Db 715 CCGATCCATGTGGACCGCGAGCGCGGGTTCATCGCGCGCTTCATCTACCCGAGGTG 774
Qy 260 GluTrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGly 279
Db 775 GAGTGGGACTTCCGGCTGCCGCTGGTGAAGAGATCAACGTCAGCGGCCCAAGTACCGG 834
Qy 280 LeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGlu 299
Db 835 CTCGTCTACCGCGCGGTGGGTGGTTCATCTGGCGCAACAAGGAGGACCTCCCGGATGAG 894
Qy 300 LeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSer 319
Db 895 CTCATCTTCCACATCAACTACTCCTCGCGCGCAGCAGCAACCTTCACGCTCAACTTCTCC 954
Qy 320 LysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeuLeuIleArgLeuGlyHisGluGly 339

955 AAAGATCGAACCCAGATAATTCGCAGCTATTACAGCTCATTCGTCTCGAATTCGAGGGG 1014

340 TyrArgAsnValMetGluAAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlu 359

1015 TACAAGGACATCATGCAGACTCGCGGACAAACGCGGTGTCTCCGGAGGGATCGAG 1074

360 LysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSer 379

1075 AAGACGGGCCCATTCGACGCTGTGTCCAAGGACTCCGCGCTGCGCGCTGGTGGCCTTCTCC 1134

380 LeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGly 399

1135 CTCAAGGACTCGTCGGGTACACGGTGTTCGAGGTGGCGGAGACCTCCGCGCTTCGGC 1194

400 TrpIleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgVal 419

1195 TGGATCGTCCGGCGGTACACCATGCGCGCCAGCGTACGACGTCGCGCTGATCGCGCTC 1254

420 ValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLys 439

1255 GTCATCCGCGAGGACTTCAGCGCGGCTTCGCCGAGGCGCTCATACCGACCTCACCAG 1314

440 ValMetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGln 459

1315 ACGGTGGCCGATATGGAC-----GCCACGCGCTC----- 1344

460 GluLysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAsp 479

1345 AAGAAAGCCGCGCGCGAG-----CGGCCAAGAAGACCGTCGCGGAG 1386

480 LysGlnArgAspIleIleThrGlyTrpLysLysPheValAlaAspArgLysLysThrSer 499

1387 ATAGAGAGGAGGTGACCACTACTGCGGAGTTCGTTCGCC---AGGAAGAAGACGAGC 1443

500 GlylleCys 502

1444 CTCGTCGTC 1452

RESULT 13

3-10-006-852-7

Sequence 7, Application US/10006852

Publication No. US20030046732A1

GENERAL INFORMATION:

APPLICANT: Kinnersely, Alan M.

APPLICANT: Turano, Frank J.

TITLE OF INVENTION: Methods for Regulating Plant GABA Production

FILE REFERENCE: 7224-65

CURRENT APPLICATION NUMBER: US/10/006,852

CURRENT FILING DATE: 2002-07-01

PRIOR APPLICATION NUMBER: US 60/246,367

PRIOR FILING DATE: 2000-11-07

NUMBER OF SEQ ID NOS: 24

SOFTWARE: PatentIn version 3.1

SEQ ID NO 7

LENGTH: 2121

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: CDS

LOCATION: (1)..(87)

OTHER INFORMATION:

FEATURE:

NAME/KEY: CDS

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FEATURE:

NAME/KEY: CDS

LOCATION: (782)..(994)

OTHER INFORMATION:

FEATURE:

NAME/KEY: CDS

LOCATION: (1081)..(1335)

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/	NAME/KEY: CDS
/	LOCATION: (1654)..(2116)
/	OTHER INFORMATION:
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Query Match:	74.05% Indels: 226
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Db	ValArgThrSerLeuPro----- 28
Qy	21 ArgTyValArgThrSerLeuPro----- 28
Db	CGTTACGTCGGCAACTCTCTTCCACGGTAACAACCTGTAAACACAAATCTTTTGTCTAATG 120
Qy	28 ----- 28
Db	121 TTTTCGTCAACAATAGTAGAACATGAATGATAAACCCTTGGATAGTTTTTTTTTTGGCGG 180
Qy	28 ----- 28
Db	181 TGGTTAATGTTGTAGATTATTATGTGTTATATACTATAAGAAGGACATGTTTCGTTAT 240
Qy	29 -----ArgPhelysMetProGluuAsnSerIlePro 38
Db	241 TTAACTTAACTGTCATCATTTTCATCATTTAGATTCGAAATGCCTGAGAACTCAAATCCA 300
Qy	39 LysGluAlaAlaty-GlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArgLeu 58
Db	301 AAAGAAGCAGCTTACCAATCATCAACGACGAGCTAATGCTCGATGTTAACCACCAAGCTG 360
Qy	59 AsnLeuAlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSer 78
Db	361 AACCTAGCTTCTCTCGTACCACTAGGATGAGGCCAGAAATGTGAAGAGCTCATGATGGAG 420
Qy	79 SerIleAsnLysAsnTyxValAspMetAspGluTyxProValThrThrGluLeuGlnAsn 98
Db	421 TCCATCAACAAGACTACGTGCACATGACGAGTACCTGTGCACCACTGAGCTTCAGAAC 480
Qy	99 ArgCysValAsnMetIleAlaHisIleuPheAsnAlaProLeuGluGluAlaGluThrAla 118
Db	481 CGATGTGTTTAAACATGATAGCACGTCTCTTCAACGCGCGCTTGGTGACGCTGAAGCTGCC 540
Qy	119 ValGlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLys 138
Db	541 GTTGGNGTTGGCACCGTCCGATCGTCCGAGGCGATTTATGTTGGCCGGTTTTGGCTTTAAG 600
Qy	139 ArgGlyTrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleVal 158
Db	601 AGACAATGGCAAGTAAGCGTAAGGCCCAAGGGCTTCTTTATGATAAGCCCAATATCGTA 660
Qy	159 ThrGlyAlaAsnVal----- 163
Db	561 ACCGGTGCTAATGTCCAGGTAAACCAAAACAAAATTTGATGAATATTAAACCAAGACAA 720
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181 GTCAACACCGAAGTCCAGG----- 200
112 LeuGluGluAlaGluThrAlaValGly-ValGlyThrValGlySerSerGluAlaIleMe 131
201 -----GACTCTGAACCGGCGTCGAAGTCGGCACTGTCTGGCTGTCTGAGGCCATCAT 254
131 tLeuAlaGlyLeuAlaPheLysArgLysTrpGlnAsnLysArgLysAlaGluLysPr 151
255 GCTCGCGGTTTGCCCTTCAAGAGAGGTGGCAACAAGATGAAGCAGCGCGCAAGCC 314
315 ATGGCACAAGCCTAACATTGTCAACGGCGCAATGTCCAAGTTTGTGGGAGAAGTTGCG 374
171 aArgTyrPheGluValGluLeuLysGluValLysLeuSerGluGlyTyrTyrValMetAs 191
375 GCGATACTTCGAGGTTGAGCTCAAGGAAGTGAAGCTGAGTGACGGCTACTACGTCAATGA 434
191 pProGlnGlnAlaValAspMetValAspGluAsnThrIleCysValAlaAspIleLeuGl 211
435 CCAGCTAAGCGCGTGATATGTGACGAGAAACCAATCTGCGTCGGCGCATCTCGG 494
211 ySerThrLeuAsnGlyGluPheGluAspValLysLeuLeuAsnAspLeuLeuValGlu 231
495 GTCAGCCTGAACGGGAGTTTCAGGAGCGTGAAGCTGCTCAACGATCTGCTACCAAGAA 554
231 sAsnLysGluThrGlyTrpAspThrProIleHisValAspAlaAlaSerGlyGlyPheIl 251
555 GAACGCTGAACAGGCTGGGACACGCCGATCCACGTGGACGCGCGGAGCGGGGTTCAT 614
251 eAlaProPheLeuTyrProGluLeuGluTrpAspPheArgLeuProLeuValLysSerIl 271
615 CGCGCGCTTCTGTACCGGAGCTGGAGTGGGACTTCCGCTCCGCTGGTGAAGAGCAT 674
271 eAsnValSerGlyHisLysTyrGlyLeuValTyrAlaGlyIleGlyTrpValIleTrpAr 291
675 CAACGTGAGCGGGCACAAGTACGGCTCGTCTACCGCGGATCGGGTGTGTCATCTGGAG 734
291 gAsnLysGluAspLeuProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaSpGl 311
735 GAGCAAGGAGGATCTGCTGAGGAGCTCATCTTCCACATCAACTACTCTCGCGCGCACCA 794
311 nProThrPheThrLeuAsnPheSerLysGlySerSerGlnValIleAlaGlnTyrTyrGl 331
795 GCCACACCTTCACCTCAACTTCTCCAAGGTTCCAGCCAGGTCAATGTCACAGTATTACCA 854
331 nLeuIleArgLeuGlyHisGluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMe 351
855 ACTAATCCGCTAGGCTTTGAGGGGGTACAAGAACATCATGAGAACTGCCAGGAGAACGC 914
351 tIleValLeuArgGluGlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGl 371
915 GATGGTCTGAGCAGGGGCTGGAGAGACGCGGCGGTTTCAACATCGTGTGCCAAGGACAA 974
371 uGlyValProLeuValAlaPheSerLeuLysAspSerSerCysHisThrGluPheGluIl 391
975 CGGCGTGGCGTGGTGCCCTTCCCTCAAGGACAGCGCGCGCACCAACGAGTTCGAGAT 1034
391 eSerAspMetLeuArgArgTyrGlyTrpIleValProAlaTyrThrMetProProAsnAl 411
1035 CTCGAGACTTCTCCGCGCTTTCGGCTGATCGTCCGCGCCTTACACCATGCCCCCGCAGCG 1094
411 aGlnHisIleThrValLeuArgValValIleArgGluAspPheSerArgThrLeuAlaGl 431
1095 GCAGCAGCTCACCGTCTCCCGCTGCTCATCCGCGAGACTTTCAGCCGCGACGCTCGCCGA 1154
431 uArgLeuValIleAspIleGluLysValMetArgGluLeuAspGluLeuProSerArgVa 451
1155 GCGCCTCGTCTCGACGTCGAGAAAGGTGCTGCACGAGTCTGCACGCGCTTCCCGCGCGCT 1214
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OY 451 lile 452
Db 1215 CGTC 1218
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RESULT 15

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US-10-167-547C-3
; Sequence 3, Application US/10167547C
; Publication No. US20030170653A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; APPLICANT: Damude, Howard G.
; TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
; FILE REFERENCE: CL1804 US NA
; CURRENT FILING DATE: 2003-03-17
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Microsoft Office 07
; SEQ ID NO 3
; LENGTH: 1530
; TYPE: DNA
; ORGANISM: Alstroemeria
US-10-167-547C-3
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Pred. No.: 3,696-207 Length: 1530
Score: 1864.00 Matches: 351
Percent Similarity: 84.55% Conservative: 54
Best Local Similarity: 73.28% Mismatches: 70
Query Match: 71.28% Indels: 4
DB: 12 Gaps: 2
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US-10-006-852-2 (1-502) x US-10-167-547C-3 (1-1530)

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Db 1 ATGGCTCTCTCCAGCGTCTCTCCGACTCCAAACCAACCAAGTGCAGTGCACCTATGCCTCT 60
OY 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
Db 61 CGCTACGTTTCGGCAGCAGGCTCCAGGTTTCAGGATGCCGAGAGAGTGCATACCAAGAGAG 120
OY 41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
Db 121 GCGGCGTTTCACGATGATCAACGACGAGCTGATGCTGGACGGGAACCCCGAGGCTGAACCTG 180
OY 61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
Db 181 GCTTCGTTTCGTCACGACGCTGGATGGACGGAGTGCATCGTCTGATGATGTTCACCATC 240
OY 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
Db 241 AACAGAACTACGCCCTCATGGACGATTACCCGGTCACTATTGACATACAGAAATCGCTGC 300
OY 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
Db 301 GTGAATATGATAGCAACCTCTTTAATCGGCAATTGGGAGGGGGGAAACCAACAGTAGGA 360
OY 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
Db 361 TGTGCTACGCTGGGATCATCAGAACCATGATGCTTTCGCGGTTGGCATTTCAAGAGAAAT 420
OY 141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
Db 421 TGCAGCAACAAGAAAGGACAGAGGGGAGGCATATGACAGCCCAACATGGTCACCGGT 480
OY 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
Db 481 TCAAAATGTTTCAGGTTTGTGGTGAAATTCGCTAAGTATTTTGAAGTTTGAATGAAAAA 540
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GenCore version 5.1.6
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1 protein - nucleic search, using frame_plus_p2n model

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direct score: 2615
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ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
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DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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4: /cgn2_6/ptodata/2/ina/6B.COMB.seq.*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

result	No.	Score	Query Match	Length DB	ID	Description
c	1	2014	77.0	1783	2	US-08-522-421-8
c	2	1114	42.6	4403765	3	US-09-103-840A-2
c	3	1114	42.6	4411529	3	US-09-103-840A-1
c	4	1025	39.2	5565	3	US-09-068-195-21
c	5	605	23.1	36941	4	US-08-311-731A-130
c	6	325	12.4	1770	4	US-08-939-309-7
c	7	325	12.4	1770	4	US-08-849-180-7
c	8	325	12.4	1770	4	US-09-356-643B-1
c	9	265.5	10.2	1629	4	US-08-939-309-5
c	10	285.5	10.2	1629	4	US-08-849-180-5
c	11	285.5	10.2	1629	4	US-08-356-643B-3
c	12	257	9.8	359	4	US-09-056-556-192

c	13	257	9.8	359	4	US-09-072-596-187	Sequence 187, Appl
c	14	246.5	9.4	1707	4	US-08-939-309-1	Sequence 1, Appli
c	15	246.5	9.4	1707	4	US-09-849-180-1	Sequence 1, Appli
c	16	246.5	9.4	1707	4	US-09-356-643B-5	Sequence 5, Appli
c	17	227	8.7	1707	4	US-08-939-309-3	Sequence 3, Appli
c	18	227	8.7	1707	4	US-09-849-180-3	Sequence 3, Appli
c	19	227	8.7	1707	4	US-09-356-643B-7	Sequence 7, Appli
c	20	225	8.6	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	21	224	8.6	2130	4	US-09-740-369-1	Sequence 1, Appli
c	22	177	6.8	3162	4	US-09-356-643B-12	Sequence 12, Appli
c	23	160.5	6.1	1467	4	US-08-939-309-9	Sequence 9, Appli
c	24	160.5	6.1	1467	4	US-09-849-180-9	Sequence 9, Appli
c	25	160.5	6.1	1467	4	US-09-356-643B-9	Sequence 9, Appli
c	26	133.5	5.1	1578	4	US-09-328-352-366	Sequence 366, App
c	27	121.5	4.6	1830121	4	US-09-557-884-1	Sequence 1, Appli
c	28	121.5	4.6	1830121	4	US-09-643-990A-1	Sequence 1, Appli
c	29	116	4.4	1944	3	US-09-377-557-19	Sequence 19, Appli
c	30	113	4.3	1197	4	US-09-328-352-381	Sequence 381, App
c	31	110.5	4.2	129908	4	US-09-585-858-1	Sequence 1, Appli
c	32	105	4.0	2190	4	US-09-134-001C-1891	Sequence 1891, Ap
c	33	105	4.0	5340	4	US-09-627-122-21	Sequence 21, Appli
c	34	105	4.0	1664976	4	US-08-916-421B-1	Sequence 1, Appli
c	35	104	4.0	3312	4	US-09-669-751-259	Sequence 259, App
c	36	104	4.0	4032	1	US-08-107-748-3	Sequence 3, Appli
c	37	104	4.0	4032	1	US-08-245-809-4	Sequence 4, Appli
c	38	104	4.0	4032	5	PCT-US92-01385-3	Sequence 3, Appli
c	39	102.5	3.9	2193	3	US-09-398-865A-1	Sequence 1, Appli
c	40	102.5	3.9	2193	4	US-09-710-714-1	Sequence 1, Appli
c	41	102.5	3.9	2992	1	US-07-718-575-1	Sequence 1, Appli
c	42	102.5	3.9	2992	1	US-08-481-206-1	Sequence 1, Appli
c	43	102.5	3.9	2992	2	US-08-486-269A-1	Sequence 1, Appli
c	44	102	3.9	1734	3	US-08-687-590-60	Sequence 60, Appli
c	45	101.5	3.9	3666	4	US-09-107-532A-305	Sequence 305, App

ALIGNMENTS

RESULT 1

US-08-522-421-8
; Sequence 8, Application US/08522421
; Patent No. 5908973
; GENERAL INFORMATION:
; APPLICANT: Abu-Bakar, Umi Kalsom
; APPLICANT: Barton, Sarah Louise
; APPLICANT: Gallego-Verigas, Pedro Pablo
; APPLICANT: Gray, Julie Elizabeth
; APPLICANT: Grierson, Donald
; APPLICANT: Lowe, Alexandra Louise
; APPLICANT: Picton, Steve
; APPLICANT: Whorton, Lee Colin
; TITLE OF INVENTION: DNA, DNA CONSTRUCTS, CELLS AND PLANTS
; TITLE OF INVENTION: DERIVED THEREFROM
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pillsbury Madison & Sutro, L.L.P.
; STREET: 1100 New York Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3918
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/522,421
; FILING DATE: 11-JAN-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9305868.3
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9305869.1
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305859.2
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305865.9
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305866.7
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305867.5
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305860.0
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9305862.6
 FILING DATE: 22-MAR-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9314351.9
 FILING DATE: 12-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9320988.0
 FILING DATE: 12-OCT-1993
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1783 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 ORIGINAL SOURCE:
 ORGANISM: ERTD1
 S-08-522-421-8

Alignment Scores:
 Seq. No.: 3,64e-239 Length: 1783
 core: 2014.00 Matches: 387
 Percent Similarity: 86.44% Conservative: 53
 Percent Local Similarity: 76.03% Mismatches: 55
 Query Match: 77.02% Indels: 14
 B: 2 Gaps: 5

S-10-006-852-2 (1-502) x US-08-522-421-8 (1-1783)

Y 1 MetValLeu---SerHisAlaValSerGluSerAspValSerValHisSerThrPheAla 19
 b 6 ATGGTGTAAACACGAGCTCGATAAGAGATTCAGAGAGAGCTTGACCTACATTGGCA 65
 Y 20 SerArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLys 39
 b 66 TCAAGATATGTACAGGAACCTTTACCTTAAGTTCAAAATGCTAAAAATCCATGCCGAAA 125
 Y 40 GluAlaIa 59
 b 126 GAACAGCCTATCATCATGTAAACGACGAGCTATGTGTGATGATGATGATGATGATGATGAT 185
 Y 60 LeuAlaSerPheValThrThrThrMetGluProGluCysAspLysLeuIleMetSerSer 79
 b 186 TTACCTTCCTTTGTAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 245
 Y 80 IleAsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArg 99
 b 246 ATTAATAAAACTATGTCACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 305
 Y 100 CysValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaVal 119
 b 306 TGTGTAACTGTTAGACATCTTTTCATGCCCGGCTTGGTGAATGATGATGATGATGATGATGAT 365
 Y 120 GlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArg 139

Db 366 GGAGTTGGTACAGTGGGTTTCATCAGAGCGCAATAATGCTTGTGTCGCTTGTCTTCAAACGC 425
 QY 140 LysTrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThr 159
 Db 426 AAATGGCAATCGAAAAAGAAAGCAGAAAGCAACCTTTTCGATAGCCTAATATAGTCACT 485
 QY 160 GlyAlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLys 179
 Db 486 GGAGCTAATGTGCAGGTTCTGCTGGGAAAAATTTCAAGGTATTTTGAAGTTGAGTTGAAG 545
 QY 180 GluValLysLeuSerGluGlyTyrValMetAspProGlnGlnAlaValAspMetVal 199
 Db 546 GAGGTGAACCTTAAAGAGGATACTATGTAATGACCCCTGCCAAGCAGTAGAGATAGTG 605
 QY 200 AspGluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGlu 219
 Db 606 GATGAGATACATATGTTGCTGCAATCTTGGTTCTACTCTGACTGGGGAGTTTGAG 665
 QY 220 AspValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThr 239
 Db 666 GATGTGAAGCTCTTAAACGAGCTCTTACAAAAGAACCAAGGAAACCGGATGGGAGACA 725
 QY 240 ProIleHisValAspAlaIaIaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeu 259
 Db 726 CCGATTCAATGTCGATGCTGCGAGTGGAGATTATTTGCTCTTCTCTGCGCAGATCTT 785
 QY 260 GluTrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGly 279
 Db 786 GAATGGGATTTCCGTTTGCCTCTTGTGAAAAAGTATAAATGTACGCGGTCAACAGTATGGC 845
 QY 280 LeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGlu 299
 Db 846 CTGTATATGCTGTGTCGGTGGTGATATGGCGAGCAAGGAACTTCCCGCATGAA 905
 QY 300 LeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSer 319
 Db 906 CTCGCTTTTCATATAAACTACCTTGGGTCTCATCAGCTACTTTTACTCTCACTCTCT 965
 QY 320 LysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGly 339
 Db 966 AAAGGTTCTCTCAATAATATGTCACAGTATATATCAGTTAATAGACTTGGCTTTGAGGGT 1025
 QY 340 TyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlu 359
 Db 1026 TATAAAGACGTCATGAAGAATTCTTATCAACCAAGAACTAACAGAGGAATCACA 1085
 QY 360 LysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSer 379
 Db 1086 AAAATGGGGCGGTTTCGATATTGTTCTTAAGGATGGGGTGTCTCTGTGTAGCATTTTCT 1145
 QY 380 LeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGly 399
 Db 1146 CTCAGGGACAGCAGCAAAATATACGGTATTTGAAGTATCTGAGCATCTCAGAAAGATTGGA 1205
 QY 400 TrpIleValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgVal 419
 Db 1206 TGGATCGTCCCTGCTATACATATGCCACCGGATGCTGACACATGCTGTACTCGGGGT 1265
 QY 420 ValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLys 439
 Db 1266 GTCAATTAGAGAGGATTTTCAGCCACAGCTAGCTGAGACTTGTCTGACATTTGAGAAA 1325
 QY 440 ValMetArgGluLeuAspGluLeuProSerArgValIleHisLysIle-----SerLeu 457
 Db 1326 ATTCTGTCAGAGTTGGACACACAGCCTCTCTGTTTGGCCCAAGCTGTCCGTGTCAC 1385
 QY 458 GlyGlnGluLysSerGluSerAsnSerAspAsnLeu-----MetValThrVal 473
 Db 1386 GCTGAGAGAGTCGTGATGACAAAGGTGATGGGCTTCATCATTTTCATCATGGATGACTGTA 1445
 QY 474 LysLysSerAspIleAspLysGlnArgAspIleThrGlyTrpLysLysPheValAla 493
 Db 1446 -----GAGACTCAGAAAGACATTTATCAACATTTGGAGAAAATCGCAGG 1490


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CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
S-09-103-840A-1

Ligment Scores:
red. No.: 6,35e-122 Length: 4411529
core: 1114.00 Matches: 219
Percent Similarity: 65.63% Conservative: 77
est Local Similarity: 48.56% Mismatches: 143
uey Match: 42.60% Indels: 12
B: 3 Gaps: 5

S-10-006-852-2 (1-502) x US-09-103-840A-1 (1-4411529)
Y 6 AlaValSerGluSerAspValSerVal-----HisSer-----ThrPheAlaSer 20
b 3851753 GCGGTGTCGCGAGTACCCTCGTCCGCGCGCATTCGATCGCTCCGGCTACACCGGT 3851694
Y 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
b 3851693 CGGATGTTCCCGCACCGCGTCCGCGCTCGGATGCGCATGAGTGGATCCCGAG 3851634
Y 41 AlaAlaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyValProArgLeuAsnLeu 60
b 3851633 GCGGCTATCGCTTCATCCAGCAGAGTGTATGCTCGACGGTAGTCTCGGCTGATCTG 3851574
Y 61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
b 3851573 GCCACCTTCGTGACCACTGGATGACCGCGAGCGCGAAAGCTGATGGCCGAGAGCTTC 3851514
Y 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
b 3851513 GACAAGAACATGATCGATGATAGGACGAATACCCGCGCACCGCGCATCGAGCGCGCTGT 3851454
Y 101 ValAsnMetIleAlaHisLeuPheAsnAlaPro-----LeuGluGluAlaGluThr 117
b 3851453 GTGTCCATGTGCGCGCACCTGTTTCAGCGCGAGGGTCTCGCGACACGACCCACCCAGC 3851394
Y 118 AlaValGlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPhe 137
b 3851393 GCCACCGGGGTGTCCACATCGGCTCCAGCGAGCGGTGATGTGGTGGGCTGGCCCTG 3851334
Y 138 LysArgLysTrpGlnAsnLysArgLysAla---GluGlyLysProValAspLysProAsn 156
b 3851333 AATGGCGTGGCGCGCAACGGTGGGTCTTGGAGGGGCGC-----ATGCCCAAT 3851283
Y 157 IleValThrGlyAlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluVal 176
b 3851282 CTGTGTATGGTGTTCGACGCTCCAGTGTGTGGGAGAGTCTCCCGCTACTTTCGAGCTC 3851223
Y 177 GluLeuLysGluValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaVal 196
b 3851222 GAACCCCGTTACCTGCGGATGGAGCGGGCGGTACGTCTATCCCGCGAGCAGGTGCTC 3851163
Y 197 AspMetValAspGluAsnValIleCysValAlaAspIleLeuGlySerThrLeuAsnGly 216
b 3851162 GCCGCGTTCGACGAGAACCATCGGTGGGTGGCGATCTTGGGCACCATATACCGGT 3851103
Y 217 GluPheGluAspValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGly 236
b 3851102 GAATCGAACCATCCCGCAGATCGCGCGCTGGCAAACTGGCGGCTGGCGGGGT 3851043
Y 237 TrpAspThrProIleHisValAspAlaAlaSerGlyPheIleAlaProPheLeuTyr 256
b 3851042 GTGACGCTCCCGGTATACGTCGACGCGCGCAGTGGGGCTTTTGTGGTCCGCTTTTGAT 3850983
Y 257 ProGluLeuGluTyrPheArgLeuProLeuValLysSerIleAsnValSerGlyHis 276

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Db 3850982 CCGGACCTGGTATGGGATTTTCGGCTGCCCGCTGGTGTGCATCAACGTCAGCGGCAC 3850923
QY 277 LysTyrGlyLeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeu 296
Db 3850922 AAGTATGGGCTGACCTATCCCGCGGTTCGGGTTCGTGTGGCGGGCCGAGACCTG 3850863
QY 297 ProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeu 316
Db 3850862 CCGGAGGATCTGGTTTCCGGGTCACTACCTCGCGCGGACATGCGGACCTTCACCGCTG 3850803
QY 317 AsnPheSerLysGlySerSerGlnValIleIleGlnTyrTrpGlnLeuIleArgLeuGly 336
Db 3850802 AACTTCTCCGTCGCGGTAAACAGGTGGTGGCGCAGTACTACAACTTCTCGCGCTGGG 3850743
QY 337 HisGluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGlu 356
Db 3850742 CCGGACGGCTATACCAAGTGTATGACGGCGCTGTGCGACACCGCGCGGTGGCTGGGTGAC 3850683
QY 357 GlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuVal 376
Db 3850682 CAGCTCGCGAGGTGGATCATTTGCGAGGTGATCTCGGATGTTGCGGATCCCGGTGTC 3850623
QY 377 AlaPheSerLeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArg 396
Db 3850622 AGCTTCCGCGCTCGCGCGGACCGCGGTGACAGGATTCGACGTTCCCATAGCTGCGG 3850563
QY 397 ArgTyrGlyTyrIleValProAlaTyrThrMetProAsnAlaGlnHisIleThrVal 416
Db 3850562 ACCTTCGGGTGGCAGGTGCCCGCTACACCATGCGGACACCGCAGCGCGGTG 3850503
QY 417 LeuArgValValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAsp 436
Db 3850502 CTGCGGATCGTGGTTCGGAAGGACTCTCCGCGACCTGGCGCGGCGCTGCACGACGAC 3850443
QY 437 IleGluLysValMetArgGluLeuAspGluLeu 447
Db 3850442 GCGGTACCGCGGTGGCTGGCTGCCCTGGACAAGGTC 3850410

RESULT 4
US-09-068-195-21
; Sequence 21, Application US/09068195B
; Patent No. 6140078
; GENERAL INFORMATION:
; APPLICANT: Sanders, Jan W.
; APPLICANT: Ledebor, Adrianus M.
; APPLICANT: Venema, Gerard
; APPLICANT: Kok, Jan
; TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid
; TITLE OF INVENTION: Bacterium, and Its Use in a Lactic Acid Bacterium for
; TITLE OF INVENTION: Production of Desired Protein
; FILE REFERENCE: Sanders-60113/025227
; CURRENT APPLICATION NUMBER: US/09/068,195B
; CURRENT FILING DATE: 1998-07-29
; EARLIER APPLICATION NUMBER: PCT/EP97/04755
; EARLIER FILING DATE: 1997-08-20
; EARLIER APPLICATION NUMBER: EP 97200744/7
; EARLIER FILING DATE: 1997-03-13
; EARLIER APPLICATION NUMBER: EP 96202444/4
; EARLIER FILING DATE: 1996-09-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 5565
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: genomic DNA of
; OTHER INFORMATION: NS3 locus containing gadRCB
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (3)..(500)
; OTHER INFORMATION: C-terminus of rhnB

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FEATURE:

NAME/KEY: mat peptide

LOCATION: (1095)..(1922)

OTHER INFORMATION: rggl = gadr

FEATURE:

NAME/KEY: mat peptide

LOCATION: (2069)..(3577)

OTHER INFORMATION: orfx = gadc

FEATURE:

NAME/KEY: mat peptide

LOCATION: (3600)..(4997)

OTHER INFORMATION: gadb

FEATURE:

NAME/KEY: mat peptide

LOCATION: Complement((5078)..(5563))

OTHER INFORMATION: C-terminus of ORF in opposite direction

S-09-068-195-21

Alignment Scores:

red. No.: 8.5e-116 Length: 5565
 core: 1025.00 Matches: 203
 core: 63.46% Conservative: 94
 est Local Similarity: 43.38% Mismatches: 156
 uery Match: 39.20% Indels: 15
 B: 3 Gaps: 4

S-10-006-852-2 (1-502) x US-09-068-195-21 (1-5565)

18 PheAlaSerArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIle 37
 3651 TTGGTTCAGAAAGTGACAGGAGGATTTACCTAAATATATTAATGACTCAACAATCAAT 3710
 38 ProLysGluAlaLalTyrGlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArg 57
 3711 GAGCTCGAGTGGCCTATCAGTTAGTCAAGATCAATGATGAGGCAACGCTCGT 3770
 58 LeuAsnLeuAlaSerPheValThrTyrMetLeuProGluCysAspLysLeuIleMet 77
 3771 TTAAATTTGGCCATCTCTCAAACTTATATGAACTTATGAACTTATGAACTTATGAACT 3830
 78 SerSerIleAsnLysAsnTyrValAspMetAspGluTyrProValThrTyrGluLeuGln 97
 3831 CAGACCTTGGAAATAAATGCGATTGACAAATCAGATATCCAGAACAACTGAAATGAA 3890
 98 AsnArgCysValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThr 117
 3891 AACCGTTGCGTCAACATGCTGCTGACCTTGGAAATGCG-----AGTGAATAAGGAAAA 3944
 118 AlavalGlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPhe 137
 3945 ATTATGGGACTTCGACAAATGGTTCTTCAGAACCTTGTATGCTTGGGGAATGGCTATG 4004
 138 LysArgLysTyrGlnAsnLysArgLysAlaGluLysProValAsp-----LysPro 155
 4005 AAGTTTCTGGCGTAAGCGAGCAGAAAAATAGGCGCTAGATATTAATGCGAAAAAGCCA 4064
 156 AsnIleValThrGlyAlaAsnValGlnValCysTyrGluLysPheAlaArgTyrPheGlu 175
 4065 AACTTAGTCAATTTCTCTGTTATCAAGTTTGTCTGGGAAAAATTTCTGTGTTATTTGGAT 4124
 176 ValGluLeuLysGluValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAla 195
 4125 ATTGAATGAGAGAGTGCCTAGATAGAACATATGCAATCAATTTGGAAAAAGTG 4184
 196 ValAspMetValAspGluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsn 215
 4185 ATGATTTATGTTGATGATATACGTTGCGATAGTATGGAATTTAGGGGATTTACTTACT 4244
 216 GlyGluPheGluAspValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThr 235
 4245 GGTGCTTATGATGATATCAAGCTTTGGTAATTTGTAAGAAATATATATAACAGACA 4304
 236 GlyTyrAspThrProIleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeu 255

Db 4305 GACTCAAAAGTTTATATTCAGTAGATGCTGCTCAGAGGACTTTATGCTCCTTTTGT 4364
 QY 256 TyrProGluLeuGluTyrAspPheArgLeuProLeuValLysSerIleAsnValSerGly 275
 Db 4365 GAGCCAGAACCTTGAGTGGGATTTCCGTTTGAAAAATGTCATTTCAATCAATACITCAGGA 4424
 QY 276 HisLysTyrGlyLeuValTyrAlaGlyIleGlyTyrValIleTyrPheAsnLysGluAsp 295
 Db 4425 CATAAATATGTTTATGATATATCCTGCTGCTAGTGGTCTTGTGGCGTGACAAAAATAT 4484
 QY 296 LeuProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThr 315
 Db 4485 TTACCTGAAGAGTTAATTTTAAAGTAAGTATCTTGGAGAGGAATTTACCAACAATGGCG 4544
 QY 316 LeuAsnPheSerLysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeu 335
 Db 4545 ATTAATTTTCTCACAGTCTTCTCAATTAATCGGTCAATACTATATAATTTGTACGTTAT 4604
 QY 336 GlyHisGluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArg 355
 Db 4605 GGATTTGATGGATATAAAGCTTATTCATGAGAGAACGCATATAAAGTAGCCATGTTATTAGCA 4664
 QY 356 GluGlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeu 375
 Db 4665 GAAGAAATTTGAAAAACAGGAATGTTGAGATTATGACGATGGCGCACCAATTACCAATT 4724
 QY 376 ValAlaPheSerLeuLysAspSerSerCysHis-----ThrGluPheGluIleSerAsp 393
 Db 4725 GTCTGCTACAAATTTAAAGAAAAATTCAAACCGTGGTGGAAATCTTTATGATTTGGCAGAT 4784
 QY 394 MetLeuArgArgTyrGlyTyrIleValProAlaTyrThrMetProProAsnAlaGlnHis 413
 Db 4785 CGTTTATTAATGAAGGAGTGGCAAGTGGCTGCTTATCCACTTCTCCAAAAATTTGAAAAAT 4844
 QY 414 IleThrValArgValValIleArgGluAspPheSerArgThrLeuAlaGluArgLeu 433
 Db 4845 GAAATCAATTCACGTTTAGTAAATTCGACGAGATTTCCGGATGAATATGGCATTTAACTAT 4904
 QY 434 ValIleAspIleGluLysValMetArgGluLeuAspGlu-LeuProSerArgValIleHi 453
 Db 4905 GTTCAAGATATCAAGAGCAATTTGATGCACATAAAGGCTCATATTTCTATTTCATCAG 4964
 QY 453 sLysIleSerLeuGlyGlnGluLysSerGluSerAsnSerAspAsnLeuMetValThrVa 473
 Db 4965 GAACCTGAAAAATA-----AAACATATGGCTTTACTCACTAA 5000
 QY 473 lLysLysSerAspIleAspLys 480
 Db 5001 AGATAAAGCGATATATCTAAG 5022

RESULT 5

US-08-311-731A-130/c
 ; Sequence 130, Application US/08311731A
 ; Patent No. 6583266
 ; GENERAL INFORMATION:
 ; APPLICANT: SMITH, DOUGLAS
 ; APPLICANT: MAO, JEN-I
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
 ; TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
 ; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
 ; NUMBER OF SEQUENCES: 411
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
 ; STREET: 600 ATLANTIC AVENUE
 ; CITY: BOSTON
 ; STATE: MASSACHUSETTS
 ; COUNTRY: USA
 ; ZIP: 02210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Maki J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
S-08-939-309-7

Ligment Scores:
red. No.: 6.54e-30 Length: 1770
core: 325.00 Matches: 122
percent Similarity: 44.53% Conservative: 98
est Local Similarity: 24.70% Mismatches: 188
uery Match: 12.43% Indels: 86
B: 4 Gaps: 20

S-10-006-852-2 (1-502) x US-08-939-309-7 (1-1770)

Y 3 LeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSerArgTyr 22
b 316 TTGAGGGGTACCGTAGAAAAGAGTACCAAGGTCAAAACATCGATCGAAGACGAACTA 375
Y 23 ValArg-----ThrSerLeuProArgPhe---LysMetProGluAsnSerIleProLys 39
b 376 ATTAGATCGGACTCTCAGTTAATGAATTTCCACAGTTGCCATCCAAATGGGATACCTCAG 435
Y 40 GluAlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsn 59
b 436 GATGATGTTATTGAGAGCTAAAT-----AAATTGAAC 468
Y 60 LeuAlaSerPheValThrThrTrpMetGluProGluCys----- 72
b 469 GACTTGTATACCATACCAATCGAAGAGGAAGGTCTCTGTCGCGTTTACCACGGT 528
Y 73 -----AspLysLeuIleMetSerSerIleAsn-----LysAsnTyr 84
b 529 GGTGATGATTGATCCACTACAAACATCGCATACGAAAAAATTCGCTTGCCATCAA 588
b 85 ValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCysValAsnMetIle 104
b 589 TTACATCCGATGCTCTTCCTCGCGTACGTAATAATGAAATCGAAGTGTCTTCATGGTT 648
b 105 AlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGlyValGlyThrVal 124
b 649 TTAAGAAATGTTAATGCCCT-----TCTGATACAGGTTGTGGTACCAACTCA 699
b 125 GlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLysTyrGlnAsnLys 144
b 700 GGTGGTACAGAAATCTTGTCTTTAGCATGCTGAGCGCTAAATGATGATGCCCTTCATCAT 759
b 145 ArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGlyAlaAsnValGln 164
b 760 CGT-----GGAATCACCAGAACCAATAATTTGCTCCCGTAATCGCACAT 804
b 165 ValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGluValLysLeuSer 184
b 805 GCTGGGTTGCAAGAGCTGTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGAT 864
b 185 GluGlyTyrTyrValMetAspProGlnAlaValAspMetValAspGluAsnThrIle 204

Db 865 CCACGCACATATCAAGTGGACCTCGGAAAAATGAAAAATTCATCAATAAGAACACAAATT 924
Qy 205 CysValAlaAspIleLeuGlySerThrLeuAsn-----GlyGluPheGluAspVal 221
Db 925 TTA-----CTGGTCGGTTCGCTCCAAACCTTCTCATGGTATGCGGATGATATT 975
Qy 222 LysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTrpAspThrProIle 241
Db 976 GAAGGATTGGGTAAA--ATAGCACAAAAATATAAA-----CTTCCCTTTA 1017
Qy 242 HisValAspAlaIleAspGlyPheIleAlaProPheLeu-----TyrPro 257
Db 1018 CACGTCGACAGTTGTCTAGGTTCTCTTTATTCTTTCATTATGGAAGAGCGTGGTTACAAA 1077
Qy 258 GluLeuGlu---TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHis 276
Db 1078 AATCTGCCATTACTTGACTTTAGAGTCCGGGAGTCACCTCAATATCATGTGACACTCAT 1137
Qy 277 LysTyrGlyLeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeu 296
Db 1138 AAATATGGAATTTGCACCAAAAGGCTCGTCAGTTATATGATATAGAAACAGCGACTTACA 1197
Qy 297 ProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeu 316
Db 1198 ATGCATCAGTATTACGTAATCTCTGCTGGACTGGCGGGTATATGGCTCTCTACATTA 1257
Qy 317 AsnPheSerLysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGly 336
Db 1258 GCAGGTCCTCAGGCTCGGTGCTATTGTCGTAGTGTGTTGGGCCACTATGGTCACATGGGT 1317
Qy 337 HisGluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGlu 356
Db 1318 GAAAATGGGTAC-----ATTAGTCGTGCCAAGAA--ATAGTCGGTGCAGCAATG 1365
Qy 357 GlyLeuGluLysThrGluArgPheAsnIle-----ValSerLysAspGluGly 372
Db 1366 AGTTTAAATAATACATCCAGGAAACATTCACAGCCTGAATATAATGGGCAACCTAGA 1425
Qy 373 ValProLeuValAlaPheSerLeuLysAspSerCysHisThrGluPheGluIleSer 392
Db 1426 TATTCACTCATTTTCATTTCCTCAAGACCTTGAACATACAC-----GAACATATCT 1476
Qy 393 AspMetLeuArgArgTyrGlyTrpIleValProAlaTyrThrMetProAsnAlaGln 412
Db 1477 GACAGGTTGTCAGAAAGGCTGGCATTTCAATGCCCTACAAAAGCCG----- 1524
Qy 413 HisIleThrValLeuArgValIleArgGluAspPheSerArgThrLeuAlaGluArg 432
Db 1525 -----GTTCCACTACACATGGCTTCACGAGA---TTGAGCGCTCAT 1563
Qy 433 LeuValIleAspIleGluLysValMetArgGluLeuAspGluLeuProSerArgValIle 452
Db 1564 GTTGTGATGATGATCTGCGACATTTTACGT----- 1593
Qy 453 HisLysIleSerLeuGlyGlnGluLysSerGluSerAsnSer 466
Db 1594 -----ACTACCGTCAAGAGTTGAAGCGCAATCAAAATCT 1629

RESULT 7
US-09-849-180-7
; Sequence 7, Application US/09849180
; Patent No. 6495359
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98055

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 FILING DATE: 04-May-2001
 APPLICATION NUMBER: US/09/849,180
 CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:
 NAME: Pepe, Jeffrey C.
 REGISTRATION NUMBER: 46,985
 REFERENCE/DOCKET NUMBER: 200116.402

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1770 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1767
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Alignment Scores:
 Seq. No.: 6,54e-30 Length: 1770
 core: 325.00 Matches: 122
 Conservative: 98
 est Local Similarity: 44.53% Mismatches: 188
 Indels: 86
 Gaps: 20

US-10-006-852-2 (1-502) x US-09-849-180-7 (1-1770)

Y	3	LeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSerArgTyr	22
b	316	TTGAGGGGTACCGTAGAAAAGGAGTCAACAAGGTCAAAACAATCGATCGAAGACGAACTA	375
Y	23	ValArg-----ThrSerLeuProArgPhe---LysMetProGluAsnSerIleProLys	39
b	376	ATTAGATCGGACTCTCAGTTAATGAATTTCCACAGTTGCCATCCCAATGGGATACCTCAG	435
Y	40	GluAlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsn	59
bb	436	GATGATGTTATTGAAGAGCTAAAT-----AAATTGAAC	468
yy	60	LeuAlaSerPheValThrThrTrpMetGluProGluCys-----	72
b	469	GACTTGATACACATACCCCAATGAAGAGGAAAGGTCTCTGGTCCGTTTACCACGGT	528
yy	73	-----AspLysLeuIleMetSerSerIleAsn-----LysAsnTyr	84
bb	529	GGTGATGATTGTATCCACTTACAAACAATCGCATACGAAAAATATTGGTGTGCCAATCAA	588
yy	85	ValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCysValanMetIle	104
bb	589	TTACATCCCGATGCTTTCTCCGCGTACGTAAAATGGAATCCGAAGTGGTTCTATGGTT	648
yy	105	AlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGlyValThrVal	124
bb	649	TTAAGAATGTTTAAAGGCCCT-----TCTGATACAGGTGTGTGTACCAACACTTCA	699
yy	125	GlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLysTrpGlnAsnLys	144
bb	700	GGTGGTACAGATCTTGCCTTTAGCATGCTGAGCGCTAAATGATGATGCCCTTCATCAT	759

QY	145	ArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGlyAlaAsnValGln	164
Db	760	CGT-----GGAATCCAGCAAGCAAAATAAATTGCTCCCGTAACGCACAT	804
QY	165	ValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGluValLysLeuSer	184
Db	805	GCTGGGTTTGACAAAGCTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGGTAGAT	864
QY	185	GluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAspGluAsnThrIle	204
Db	865	CCAACGACATATCAAGTGGACCTGGGAAAAGTGAATAATTCATCAATAAGACACAAT	924
QY	205	CysValAlaAspIleLeuGlySerThrLeuAsn-----GlyGluPheGluAspVal	221
Db	925	TTA-----CTGGTGGTTCCGCTCCAAACTTTCCTCATGCTATTGCCGATGATATT	975
QY	222	LysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTyrAspThrProIle	241
Db	976	GAGGATTGGTAAA---ATAGCACAAAAATATAAA-----CTTCCTTTA	1017
QY	242	HisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeu-----TyrPro	257
Db	1018	CACGTCGACAGTTGCTAGTTCCTTTATTGTTTATGTTTATGAAAAAGGCTGGTTACAAA	1077
QY	258	GluLeuGlu---TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHis	276
Db	1078	AATCTGCCATTACTTGACTTTAGAGTCCCGGAGTCACCTCAATATCATGTGACACTCAT	1137
QY	277	LysTyrGlyLeuValTyrAlaGlyIleGlyTyrValIleTyrArgAsnLysGluAspLeu	296
Db	1138	AAATATGATTGTGCACAAAAGGCTCGTCAGTTTAAATGTTATAGAAACAGGACTTACGA	1197
QY	297	ProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeu	316
Db	1198	ATGCATCAGTATTACGTAAATCCTCTTGGAGTGGCGGTATATGGCTCTCTCTACATTA	1257
QY	317	AsnPheSerLysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGly	336
Db	1258	GCAGGGTCCAGGCTCGTCTATTGTCAGTGTGTCGGCCACTATGCTCAACATGGGT	1317
QY	337	HisGluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGlu	356
Db	1318	GAAATGGGTAC-----ATTGAGTCGTGCCAAGAA---ATAGTCGTGCCACCAATG	1365
QY	357	GlyLeuGluLysThrGluArgPheAsnIle-----ValSerLysAspGluGly	372
Db	1366	AAATTAAAAAATAACATCCAGGAAAAACATTCCAGACCTGAATATAATGGGCAACCTAGA	1425
QY	373	ValProLeuValAlaPheSerLeuLysAspSerSerCysHisThrGluPheGluLeuSer	392
Db	1426	TATTCAGTCATTTCATTTTCTTCAAGACCTTGAACATACAC-----GAATCTCT	1476
QY	393	AspMetLeuArgArgTyrGlyTyrIleValProAlaTyrThrMetProProAsnAlaGln	412
Db	1477	GACAGTTTCCAGAAAGGCTGGCATTTCAATGCCCTACAAAACCGG-----	1524
QY	413	HisIleThrValLeuArgValValIleArgGluAspPheSerArgThrIleuAlaGluArg	432
Db	1525	-----GTTGCACATACATGCGCTTCACGAGA---TTGAGCGCTCAT	1563
QY	433	LeuValIleAspIleGluLysValMetArgGluLeuAspGluLeuProSerArgValIle	452
Db	1564	GTTGGATGAGATCTGCGACATTTTACGT-----	1593
QY	453	HisLysIleSerLeuGlyGlnGluLysSerGluSerAsnSer	466
Db	1594	-----ACTACCGTCAAGAGTTGAAGACGGAATCAAAATCTCT	1629

RESULT 8

US-09-356-643B-1

; Sequence 1, Application US/09356643B

; Patent No. 6589666

ZIP: 98104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,309
 FILING DATE: 29-SEP-1997

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: David, Maki J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 200116.402

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1629 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1626

US-08-939-309-5

Alignment Scores:

red. No.:	1,34e-22	Length:	1629
core:	265.50	Matches:	118
Percent Similarity:	41.41%	Conservative:	99
Best Local Similarity:	22.52%	Mismatches:	209
Query Match:	10.15%	Indels:	98
DB:	4	Gaps:	22

US-10-006-852-2 (1-502) x US-08-939-309-5 (1-1629)

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3 LeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSerArgTyr 22
|||||
229 CTAACGAAGTAAAGGACGAGCTTGAGAAAAGCTGGAATTTGGAGTCAAGACCGAA 288
23 ValArgThrSerLeuProArgPheLysMetProLysnSerIleProLysGluAlaAla 42
|||||
289 TACTTCACATCAATCCCAAGCCATTCAGTTGGAAGAACTGAAGTACTCGCTTGCTGCC 348
43 ---TyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeuAla 61
|||||
349 ATCTATGATGATTGGAAGGACCAAGCTTTTGGGAAGG-----AGAGTATCTGGAGCA 402
62 SerPhe-----Val 64
403 GTCTTCAATAGAGAAGACGACAGGACGACGCGGAGATGATGAGGAGGTGTTCCGAAAA 462
65 ThrThrTrpMetGluProGluCysAspLysIleMetSerSerIleAsnLysAsnTyr 84
|||||
463 TTGCGCTGGACCAACCACTTGGCCAAAATTG-----495
85 ValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCysValAsnMetIle 104
|||||
496 -----TTCCCTGGAGTGAGATCATGAGGCGGTGAAGTTGTTCGCATGTGT 540
105 AlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGlyValGlyThrVal 124
|||||
541 TGTAATATGATCAATGGA-----GATTTCGGAGACATGT-----GGAACATATGTCAACT 588
125 GlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLysTrpGlnAsnLys 144
|||||
589 GGTGATCATTTCAATTCCTTGGCGTGGCTGCATCGT-----AATCGT 636
145 ArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGlyAlaAsnValGln 164
|||||
637 CTTTGAAGAGGAGGAAAGTACACAG-----ATGATTGTCCCATCATCGTCCAT 690

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QY 165 ValCysTrpGluIysPheAlaArgTyrPheGluValGluLeuLysGluValLysLeuSer 184
Db 691 GCAGCGCTTCTCAAAGCTGCCGAATGTTCCGATCAAAAGTTCGCAAGATCCAGATTGAT 750
QY 185 GluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAspGluAsnThrIle 204
Db 751 CCTGTTACTTTCAAAGTAGACCTTGTCAAATGAAGCGCGCAATTAAACAAGAGAACA-- 807
QY 205 CysValAlaAspIleLeuGlySerThrLeuAsn-----GlyGluPheGluAspVal 221
Db 808 TGTATG-----TTAGTTGGATCTGCTCAAACTTTCATTTGGAACTGTTGATGACATT 861
QY 222 LysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrProIle 241
Db 862 GAAGCTATTGGACAGCTAGCACTTGA-----TATGACATCCAGTT 903
QY 242 HisValAspAlaSerGlyGlyPheIleAlaProPheLeu---TyrProGluLeuGlu 260
Db 904 CATGTTGATGCTTGTGTTGTTGTTTCTTCTTCCATTCCTTGAAGACGAGATTGCG 963
QY 261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
Db 964 TATGACTTCCGTTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1023
QY 281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeu 300
Db 1024 GCTCCAAAGGGGTATCATGTTGTTTCTTATGCAATAAGGAACCTTCTTATATCATGAT 1083
QY 301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
Db 1084 TTCTGTGATGCTGATTGGCAAGGAGTATCTATGATCGGCTACTATGGAAGATCAGCC 1143
QY 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
Db 1144 GCTGGGCACACATTCGACTTTGCTGGCGCGCAATGCTTTATCACGCTCAGGAAGGATAC 1203
QY 341 -----ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGlu 356
Db 1204 AAGGCCAATGCTAGAAAGATTGTTGACATCAAGAAG-----ATTAGAAAT 1251
QY 357 GlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuVal 376
Db 1252 GGACTTTCAAAATTAAGGAATCAAAATTAAGGGCCAAAGTAT---GTTTGTATTGTT 1308
QY 377 AlaPheSerLeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArg 396
Db 1309 AGCTGGACAAACCAATGATGAGTT-----GAACCTACAGATTCCATAACTTCATGAAG 1362
QY 397 ArgTyrGlyTrpIleValProAlaTyrThrMetProAsnAlaGlnHisIleThrVal 416
Db 1363 GAAAAACATTTGCAACTGAATGAGCTTCAATTCCAGCTGGAGTT---CATATCATGTGTC 1419
QY 417 -LeuArgValValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAs 436
Db 1420 ACTATGAATCAT-----CTCATCTCTGA 1443
QY 436 pIleGluLysValMetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSe 456
Db 1444 CTCGCTGAAGCTTTCGTCGCGGATTGACAGCTG-----CAGTTGAG 1485
QY 456 rIeuGlyGlnGluLysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSe 476
Db 1486 TTTGTCAAAA-----GCCAAACCATCCGGAATCCGAACAGCAAGATGAACAGCC 1536
QY 476 rAspIleAspLysGlnArgAspIleIleThrGlyTrpLysLysPheValAlaAspArgLy 496
Db 1537 ATCTACGAGCTTG-----CTCAAAGTATTCCAGACCAATCGCTT 1575
QY 496 sLysThrSer 499
Db 1576 GTTCACGAGT 1585

```

ESULT 10

S-09-849-180-5

Sequence 5, Application US/09849180

Patent No. 6495359

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98055

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/849,180

FILING DATE: 04-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Pepe, Jeffrey C.

REGISTRATION NUMBER: 46,985

REFERENCE/DOCKET NUMBER: 200116.402

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 1629 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1626

SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-09-849-180-5

Alignment Scores:

Pred. No.: 1.34e-22 Length: 1629

Score: 265.50 Matches: 118

Percent Similarity: 41.41% Conservative: 99

Best Local Similarity: 22.52% Mismatches: 209

Query Match: 10.15% Indels: 98

Gaps: 22

US-10-006-852-2 (1-502) x US-09-849-180-5 (1-1629)

3 LeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSerArgTyr 22

229 CTTAAACGAAGTAAAGGACGACGCTTGAGAAAGCTGAGAAATTTGGGATCGAAGACCCGAA 288

23 ValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGluAlaAla 42

289 TACTTCACTAATCCCAAGCCATTGAGTGGGAGAACTGAAGTACTTCGCCTTGTCTGCC 348

43 ---TyrGlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeuAla 61

349 ATCTATGATGATTGGAGGACGACGCTTTTGGAGGA-----AGAGTATCTGGAGCA 402

62 SerPhe-----Val 64

403 GTCTTCAATAGAGAGACGACAGGACGAGGATGATGAGGAGGTGTTTCGGAATA 462

65 ThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIleAsnLysAsnTyr 84

Db 463 TTTGGCTGGACCAACCCACTTTTGGCCAAATGT----- 495

QY 85 ValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCysValAsnMetIle 104

Db 496 -----TTCCCTGGAGTGAAGATCATGGAGGCTGAAGTTGTTCCGCAATGTGT 540

QY 105 AlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGlyValGlyThrVal 124

Db 541 TGTAAATATGATGAATCGA-----GATTGGAGACATGT---GGAACATGATGCAACT 588

QY 125 GlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLysTrpGlnAsnLys 144

Db 589 GGTGATCCATTTCATTCTTTTGGCGCCCGGCTCATCGT-----AATCGT 636

QY 145 ArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGlyAlaAsnValGln 164

Db 637 CTTTTCMAAAGAGAGAGAAAGTACACAGAG-----ATGATTGTCCCATCCTCCAT 690

QY 165 ValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGluValLysLeuSer 184

Db 691 GCAGCGTTCTTCAAAGCTGCCGATGTTTCCGATATCAAAGTTCCGAAGATTCACATTCAT 750

QY 185 GluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAspGluAsnThrIle 204

Db 751 CTGTGTACTTTCAAAGTAGACCTTGTCAAAATGAAGCGGCAATTAAACAGAGAACA--- 807

QY 205 CysValAlaAspIleLeuGlySerThrLeuAsn-----GlyGluPheGluAspVal 221

Db 808 TGTATG-----TTAGTTGATCTGCTCCAAACTTTCCATTTTGGAACTGTTGATGACAT 861

QY 222 LysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrProIle 241

Db 862 GAAGCTATTGGACAGCTAGGACTTGAA-----TATGACATCCCATGTT 903

QY 242 HisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeu---TyrProGluPheGlu 260

Db 904 CATGTTGATGCTGTCTGTGGTGTTTCTCTTCATTCCTTGAAGACGAGATTCGC 963

QY 261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280

Db 964 TATGACTTCCGGTGTCTGTGTTCTGATCTTCGATTTCTGCAGATAGTACACAAATACG 1023

QY 281 ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300

Db 1024 GCTCCAAAGGGGTGATCATGTTCTTTATCGCAATAAGAACTTCTTCATATCAGTAC 1083

QY 301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320

Db 1084 TTCTGTGATGCTGATGGCAAGGATGATCTATGATCGGCTACTATGGAAGATTCACGC 1143

QY 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340

Db 1144 GCTGGGCACACATTCGACTTTTGGGCGCGCAATGCTTTATCAGCTCAGGAAGATAC 1203

QY 341 -----ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGlu 356

Db 1204 AAGGCCAATGCTAGAAAGATTTGTGACACTACAGAAAG-----ATTAGAAT 1251

QY 357 GlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuVal 376

Db 1252 GCATTTCAAACATTAAAGGAATCAATTTACAGGGCCCAAGTGAT---GTTTGTATTGTT 1308

QY 377 AlaPheSerLeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArg 396

Db 1309 AGCTGGACAAACCAATGATGGAGTT-----GAACCTACAGATTCATAACTTCATGAAG 1362

QY 397 ArgTyrGlyTrpIleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrVal 416

Db 1363 GAAAAACATTGGCAACTGAATGGACTTCAATTCACGCTGGAGTT---CATATCATGGTTC 1419

QY 417 -LeuArgValValIleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAs 436

456 rLeuGlyGlnGluSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSe 476
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1486 TTTGTCAAAA-----GCCACAAACCATCGGAATCCGACAAAGCAAGTGAAGCGC 1536
476 rAspIleAspLysGlnArgaspIleThrGlyTrpLysLysPheValalaAspArgLy 496
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1537 ATCTACGGATTG-----CTCAAAAGTATTCCAGACCGATCGCTT 1575
496 sLysThrSer 499
1576 GTTCACGAGT 1585

RESULT 12
S-09-056-556-192/c
Sequence 192, Application US/09056556
Patent No. 6350456
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND
NUMBER OF SEQUENCES: 241
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/056,556
FILING DATE: 07-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.457
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-056-556-192

Alignment Scores:
Pred. No.: 1.17e-22 Length: 359
Score: 257.00 Matches: 44
Percent Similarity: 61.32% Conservative: 21
Best Local Similarity: 41.51% Mismatches: 41
Query Match: 9.83% Indels: 0
Gaps: 4
DB:

US-10-006-852-2 (1-502) x US-09-056-556-192 (1-359)

280 LeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGlu 299
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359 CTGACCTATCCGGCGTGGTGGTGGCGGGCCCGGAGACCTTCCCGAGCAT 300
300 LeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSer 319
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299 CTGGTTTCCGGGTCACTACTCTCGGGCGGACATCGGACCTTCCACCTTCTCC 240
DB:

320 LysGlySerSerGlnValIleAlaGlnTyrTyrGlnIleuLleArgLeuGlyHisGluGly 339

Db 239 COTCCCGGTAAACACAGTGGTGGGCCAGTACTACAACTCTCTCGCGCTGGGGCGCACGCGC 180
:::|||||:::|||||:::|||||:::|||||:::|||||
QY 340 TyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGlu 359
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Db 179 TATACCAAGGTGATCGACGGCGTGTCCGACACCGCCCGTGGTGGGTGACACAGTGGCGC 120
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QY 360 LysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValalaPheSer 379
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Db 119 GAGGTGGATCATTTGGAGTGATCTCGGATGTTCCGGCATCCCGTGTGTGACCCCGGAC 60
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QY 380 LeuLysAspSerSerCys 385
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Db 59 ACACGCCACGCCAGTGC 42

RESULT 13
US-09-072-596-187/c
Sequence 187, Application US/09072596
Patent No. 6458366
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Dillon, Davin C.
APPLICANT: Campos-Neto, Antonia
APPLICANT: Houghton, Raymond
APPLICANT: Vedvick, Thomas S.
APPLICANT: Twardzik, Daniel R.
APPLICANT: Lodes, Michael J.
APPLICANT: Hendrickson, Ronald C.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 350
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/072,596
FILING DATE: 05-MAY-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.417C9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-072-596-187

Alignment Scores:
Pred. No.: 1.17e-22 Length: 359
Score: 257.00 Matches: 44
Percent Similarity: 61.32% Conservative: 21
Best Local Similarity: 41.51% Mismatches: 41
Query Match: 9.83% Indels: 0
Gaps: 4
DB:

US-10-006-852-2 (1-502) x US-09-072-596-187 (1-359)

QY 280 LeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluGlu 299

353 valLeuArgGluGlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGly 372
1285 TTCTCGAAGTCAGAACTGGAAACATCAAAACATCTTCAATTTTCGGT---GATCCTCAA 1341
373 valProLeuValAlaPheSerLeuLysAspSerCysHisThrGluPheGluIleSer 392
1342 TTGTCAGTTATGCTCTGGGATCCAGCATTTGACATT-----TACCGACTATCT 1392
393 AspMetLeuArgArgTyrGlyTyrIleValProAlaTyrThrMetProAsnAlaGln 412
1393 AATATGATGTCGCTAAGGGTGGAAATTTT---AATACCTGCAGTTCCCAAGAAGCAATT 1449
413 HisIleThrValLeuArgValValIleArgGluAspPheSerArgThrLeuAlaGluArg 432
1450 CATTCTGCATTAGTTAGTACATCTCGG-----AAGCGA 1485

RESULT 15

S-09-849-180-1

Sequence 1, Application US/09849180

Patent No. 6495359

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

Zhou, Jianhui

TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE

POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND

METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98055

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/849,180

FILING DATE: 04-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Pepe, Jeffrey C.

REGISTRATION NUMBER: 46,985

REFERENCE/DOCKET NUMBER: 200116.402

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1707 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1704

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

JS-09-849-180-1

Alignment Scores:

Align. No.: 3.27e-20

Score: 1707

Matches: 100

Conservative: 76

Mismatch: 210

Indels: 45

Gaps: 12

US-10-006-852-2 (1-502) x US-09-849-180-1 (1-1707)

QY 22 TyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGluAla 41
Db 334 TATGTGAAACT-----CTGCCTGCTCAGGTATGGGCACAGCTGAG 375
QY 42 AlaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeuAla 61
Db 376 GTTCTGGAGAGACTCAAGGAGTACAGCTCCATGGATGTTCTCTGGCAAGAAAGGGAAGCC 435
QY 62 SerPheValThrThrTyrMetGluProGluCysaspLysLeuIleMetSerSerIleAsn 81
Db 436 TCAGGAGCTGTGTAACAATGGGAACCGAAGCTCACGGAGCTGCTGGTCAGGCTTATCGA 495
QY 82 Lys-----AsnTyrValAspMetAspGluTyrProValThrThrGluLeuGln 97
Db 496 GAATTCACGTGGAGCAATCCACTGCATCCAGATATCTTCCCTGGATTGGGAAGTTAGAG 555
QY 98 AsnArgCysValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThr 117
Db 556 GCAGAAATCGTTAGGATGACTTGTTCCTCTTCAATGGG-----GGACCAGAT 603
QY 118 AlaValGlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPhe 137
Db 604 TCTGTGGATGTGACTTCTGGGGAACGGAAGCATCTGATGGCTGCAAGCTTAC 663
QY 138 LysArgLysTrpGlnAsnLysArgLysAlaGluLysProValAspLysProAsnIle 157
Db 664 -----CGGACTTGGCGTTAGAGAAGGGGATCAAAATCCAGAAATT 705
QY 158 ValThrGlyAlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGlu 177
Db 706 GTGGCTCCGAGAGTGCCTATGCTCATTCGACAAAGCAGCTCATTTATTTGGGATGAAG 765
QY 178 LeuLysGluValLysLeuSerGluGlyTyrTyrValMetAspProGluGlnAlaValAsp 197
Db 766 ATGTCCGAGTTGCTGAAAAGAACATGGAGGTG---GATGTCAGGCAATGAAGAGA 822
QY 198 MetValAspGluAsnThrIleCysValAlaAspIleLeuGlySerThrIleAsnGlyGlu 217
Db 823 GCCATCTCCAGGAACACAGCTATGCTGTCTTCTACCCACAGCTTCTCATGCTGTG 882
QY 218 PheGluAspValLysLeuLeuAsnAspLeuLeuValGluLysAsnLysGluThrGlyTrp 237
Db 883 ATGGATCTCTGTCCTCCGAAAGTGAACGTGTCAG-----TAT 924
QY 238 AspThrProIleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeu----- 255
Db 925 AAAATCCCACTCCATGTGGATGCTGTCTGGGGGGCTTCTCATTTCTTCAAGAGAA 984
QY 256 -----TyrPro---GluLeuGluTrpAspPheArgLeuProLeuValLysSerIleAsn 272
Db 985 GCAGGGTACCCACTGGAGAAACCATTTGATTTCCGGGTGAAAGGTGTGACCAGCATTTCA 1044
QY 273 ValSerGlyHisLysTyrGlyLeuValTyrAlaGlyIleGlyTrpValIleTrpArgAsn 292
Db 1045 GCAGATACTCATAAGTATGGCTATGCTCTAAAGGTTCATCAGTCGTGATGACTCTAAC 1104
QY 293 LysGluAspLeuProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnPro 312
Db 1105 GAGAAGTACAGGACGTACCATCTTTTGTGTGGTCAGACTGGCAAGGTGGTGTCTTACCGA 1164
QY 313 ThrPheThrLeuAsnPheSerLysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeu 332
Db 1165 TCTCAAGCATAGCTGGCTCACGGCTGGTGCATCATTTGCAGCCTGTTGGCGGCGCTTG 1224
QY 333 IleArgLeuGlyHisGluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMetIle 352
Db 1225 ATGCACCTTCGGTGAGAACCGCTATGTTGAAGTACTACCAACAGATCATCAAACTCTCTCGC 1284
QY 353 ValLeuArgGluGlyLeuGluLysThrGluArgPheAsnIleValSerLysAspGluGly 372

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

MM protein - nucleic search, using frame_plus_p2n model

run on: October 22, 2003, 15:08:39 ; Search time 358 Seconds
(without alignments)
3785.246 Million cell updates/sec

title: US-10-006-852-2
effect score: 2615
sequence: 1 MWLSHAVSESDVSHSTFAS.....DIITGKKFKVDRKKTSGIC 502

coring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Zgapop 6.0 , Zgapext 7.0
Delop 6.0 , Delext 7.0

searched: 2552756 seqs, 1349719017 residues

total number of hits satisfying chosen parameters: 5105512

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Maximum Match 0%

Listing first 45 summaries

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DB=N Geneseq 19Jun03 -CPMT=fastap -SUFFIX=ring -MINMATCH=0 -LOOPEL=0
LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human4.0.cdi
LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
MODE=LOCAL -OUTFWT=ptc -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
USFR=US10006852 @CGN 1 1 490 @runat_21102003_164103_2443 -NCPU=6 -ICPU=3
NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGIOG
DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

N Geneseq 19Jun03.*
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25: /SIDSI/gcgdata/geneseq/geneseq-nb1/NA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2615	100.0	1509	24	AAL43410	A thaliana GAD1 co
2	2607	99.7	1509	24	ABZ14005	Arabidopsis thalia
3	2240	85.7	1705	24	AAL43415	Tobacco GAD1 codin
4	2225	85.1	1784	24	AAL43417	Petunia GAD1 coding
5	2199	84.1	1771	24	AAL43416	Tobacco GAD2 codin
6	2135.5	81.7	1482	24	ABZ13132	Arabidopsis thalia
7	2130	81.5	1665	24	AAL43411	A thaliana GAD2 co
8	2014	77.0	1783	15	AAQ74691	Early Ripening Tom
9	2014	77.0	1783	24	AAL43418	Tomato GAD coding
10	1965	75.1	1605	21	AAC36324	Arabidopsis thalia
11	1936.5	74.1	2121	24	AAL43413	A thaliana GAD4 co
12	1836	70.2	1180	22	AAI70004	Tomato glutamate d
13	1834.5	70.2	2493	24	AAL43412	A thaliana GAD3 co
14	1782	68.1	1946	24	AAL43414	A thaliana GAD5 co
15	1570	60.0	1607	21	AAC44889	Arabidopsis thalia
16	1318	50.4	1545	22	AAH23436	Aspergillus oryzae
17	1236	47.3	2243	22	AAH23435	Aspergillus oryzae
18	1114	42.6	4403765	22	AAI99683	Mycobacterium tube
19	1114	42.6	4411529	22	AAI99682	Mycobacterium tube
20	1028	39.3	2365589	24	ABA90521	Genomic sequence o
21	1025	39.2	5565	19	AAV11905	L. lactis N93 locu
22	971	37.1	684707	24	ABQ67196	Listeria innocua D
23	971	37.1	3011208	24	ABQ67195	Listeria innocua D
24	959.5	36.7	2742	24	ABQ69218	Listeria monocytog
25	959.5	36.7	6077	24	ABQ71043	Listeria monocytog
26	958.5	36.7	2944528	24	ABA03041	Listeria monocytog
27	955.5	36.5	1389	24	ABQ69870	Listeria monocytog
28	955.5	36.5	2944528	24	ABA03041	Listeria innocua C
29	950	36.3	684707	24	ABQ67196	Listeria innocua C
30	950	36.3	3011208	24	ABQ69245	Listeria innocua D
31	949	36.3	4182	24	ABQ70867	Listeria monocytog
32	934	35.7	742	19	AAV28662	Ripening banana pu
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34	697	26.7	3129	23	AA81862	DNA encoding novel
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36	697	26.7	3129	23	AA92819	DNA encoding novel
37	685	26.2	416	25	ABX62354	Arabidopsis thalia
38	620.5	23.7	440	24	ABL94157	Arabidopsis thalia
39	570	21.8	960	24	ABQ75967	Yeast DNA sequence
40	545	20.8	387	25	ABX19421	Human GDP-mannose
41	508.5	19.4	1930	23	AA81857	DNA encoding novel
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43	504	19.3	3468	23	AA899926	DNA encoding novel
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45	504	19.3	3944	23	AA888584	DNA encoding novel

ALIGNMENTS

RESULT 1
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ID AAL43410 standard; cDNA; 1509 BP.
XX AAL43410;
AC AAL43410;
XX
XX
DT 25-SEP-2002 (first entry)
XX
DE A thaliana GAD1 coding sequence.
XX
XX
KW GAD; plant GABA production regulation; glutamic acid decarboxylase;
XX plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ss.
XX Arabidopsis thaliana.
XX
XX
FH Key Location/Qualifiers
FT CDS 1..1509

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WO200238736-A2.

16-MAY-2002.

07-NOV-2001; 2001WO-US47447.

07-NOV-2000; 2000US-246367P.

(EMER-) EMERALD BIOAGRICULTURE CORP.

Kinnersley AM, Turano FJ;

WPI; 2002-490073/52.

P-PSDB; AAO15132.

Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome

Claim 18; Page 53; 63pp; English.

The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAD), to provide a transformed plant that expresses the GAD coding sequence in response to a signal. Plants of this type have an enhanced ability to tolerate environmental or other stresses. The present sequence is the A. thaliana GAD1 coding sequence.

Sequence 1509 BP; 433 A; 321 C; 385 G; 370 T; 0 other;

Alignment Scores:

Record No.:	2.3e-262	Length:	1509
Score:	2615.00	Matches:	502
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

us-10-006-852-2 (1-502) x AAL43410 (1-1509)

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21	ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu	40
61	CGTTACGTCGCTACTTCCATCTCTAGCTTCAAGATGCGGAAATCGATTCTTAAGAA	120
41	AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu	60
121	CGCGCGTATCAGATCATCAAGCAGCTGATGCTTACCGGAATCCACGGTGAACCTTA	180
61	AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle	80
181	GCCTCCCTTGTGACGACATGATGAGCGCTGAGTGTGATTAACCTCATCTCTCCATC	240
81	AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys	100
241	AACAAGAACTATGTTGACATGACGAGGTACCCCGTACCCCGAACTTCAGAACCGATGT	300
101	ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGlnGluAlaGluThrAlaValGly	120
301	GTGAACATGATGTGACATCTATTCAATGCAACCGTTAGAGAGCGCGAGACCGCTCGGA	360
121	ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys	140

Db	361	GTAGGAACCGTTGGATCATCGGAGGCCATAATGTTGGCGGGTTTCGCCCTTCAAGCGTAAA	420
QY	141	TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly	160
Db	421	TGGCAGAACACAGCGCAAGCTGAGGCAAAACCGTCGATAAAACCAACATTGTCAACCGA	480
QY	161	AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu	180
Db	481	GCCAAATGTTCAAGTGTGTTGGGAGAAATTCGTAGTACTTTGAGGTTGAACCTTAAGAA	540
QY	181	ValLysLeuSerGluGlyTyrTrpValMetAspProGlnGlnAlaValAspMetValAsp	200
Db	541	GTGAATTTGAGTGAAGGATACATGTGTGATGGACCTCAACAAGCTGTGATATGGTTGAT	600
QY	201	GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp	220
Db	601	GAGAACACCATTTGTGTCGGACATCTTGTGTCCTACTCTTAATGGAGAAATTCGAAGAT	660
QY	221	ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro	240
Db	661	GTTAAACTCTTGAACGATCTCTTGGTCGAAAGAAACAAAGAAACCGGATGGGATACACCA	720
QY	241	IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu	260
Db	721	ATCCAGCTGGATCGGCAAGTGGAGATTCAATGGACCGTTTTTGTATCCGGAATTGGAA	780
QY	261	TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu	280
Db	781	TGGGACTTTAGACTTCCCTTGGTGAAGAGTAGTCAATGTGAGTGTCAACAAGTATGGACTT	840
QY	281	ValTyrAlaGlyIleGlyTrpValIleTrpArgAsnLysGluAspLeuProGluLeu	300
Db	841	GTTGACGCGAGGATTTGGTGGGTGATCTGGAGAAACAAAGAGGATTTGCCTGAGAACTC	900
QY	301	IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys	320
Db	901	ATCTTCCATATCAATATCTTGGTGTGACCAACCCACTTTACTCTCAATTTCTCCAAA	960
QY	321	GlySerSerGlnValIleAlaGlnTyrTrpGlnLeuIleArgLeuGlyHisGluGlyTyr	340
Db	961	GGTTCAAGTCAAGTCATCTGCTCAATACTACCAACTATTCGAGTGGCCACGAGGTTAC	1020
QY	341	ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys	360
Db	1021	AGAAATGTGATCGAGAAATTCAGAGAGATATGATCGTCTTAAGGGAAGGACTTCGAGAG	1080
QY	361	ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu	380
Db	1081	ACAGAAAGGTTCAACATCGTCTCAAGGACGAGGAGTGCCACTTGTGCTTTCTCCTTG	1140
QY	381	LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr	400
Db	1141	AAAGATAGCAGCTGTACACTGAGTTGCAAAATCTCCGACATGCTTCGAGGTATGGATGG	1200
QY	401	IleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgValVal	420
Db	1201	ATAGTCCCGGCTTACAAATGCTCCAAATGTCACAAACATCACCTGCTTCGTGTGGTT	1260
QY	421	IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal	440
Db	1261	ATCAGAGAAGATTTCTCGAAGACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG	1320
QY	441	MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu	460
Db	1321	ATCGGTGAGCTCGATGAGCTTCCCTTCGAGAGTATTCACAAATATCACTTGGACAAGAG	1380
QY	461	LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys	480
Db	1381	AAGAGTGAATCTAACAGCGGATTAACCTTGTGTCACGGTGAAGAGAGCGGATATCAGCAAG	1440
QY	481	GlnArgAspIleIleThrGlyTrpLysLysPheValAlaAspArgLysLysThrSerGly	500
Db	1441	CAGAGAGATATCATCTGCTGTGGAAGAAGTTTGTGCGCGACGAGAGACGAGTGGT	1500

Y 501 IleCys 502
b 1501 ATCTGC 1506

ESULT 2
BZL14005
D ABZ14005 standard; DNA; 1509 BP.
X
X
X C
X C
T T
X T
X T
E Arabidopsis thaliana stress regulated gene SEQ ID NO 1810.
X Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
X Arabidopsis thaliana.
X Arabidopsis thaliana.
X
N WO200216655-A2.
X
X 28-FEB-2002.
X 24-AUG-2001; 2001WO-US26685.
X 24-AUG-2000; 2000US-227866P.
R 26-JAN-2001; 2001US-264647P.
R 22-JUN-2001; 2001US-300111P.
X (SCRI) SCRIPPS RES INST.
X (SYGN) SYNGENTA PARTICIPATIONS AG.
X
X Harper JF, Kreps J, Wang X, Zhu T;
I WPI; 2002-304127/34.
X
X Identifying a stress condition to which a plant cell has been exposed
X and producing plants with increased tolerance to these abiotic stresses
X -

Claim 144; SEQ ID NO 1810; 577pp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:
C (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and
C (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.
C Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

X Sequence 1509 BP; 432 A; 322 C; 385 G; 370 T; 0 other;

Alignment Scores:
Aligned. No.: 1,57e-261 Length: 1509
Score: 2607.00 Matches: 501
Percent Similarity: 99.80% Conservative: 0
Local Similarity: 99.80% Mismatches: 1
Query Match: 99.69% Indels: 0
DB: 24 Gaps: 0

US-10-006-852-2 (1-502) x ABZ14005 (1-1509)

1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
1 ATGGTGCTCTCCACCGCGTATCGGATCGGATCGCTCCCTCCACTCCACATTCGCATCA 60

QY 21 ArgTyrValArgThrSerLeuProArgPheIysMetProGluAsnSerIleProIysGlu 40
DB 61 CGTTACGTCGCTACTTCTCCTAGGTTCAAGATGCCGAAACTCGAATTCCTAAGGAA 120
QY 41 AlaAlaTyrGlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
DB 121 GCGGCTATCAGATCATCAACGACGAGCTGATGTTGACGGGAATCCACGGTTGAACTTA 180
QY 61 AlaSerPheValThrThrTyrMetGluProGluCysAspIysLeuIleMetSerSerIle 80
DB 181 GCCTCCTTTGTGACGACATGGATGGAGCCTGAGTGTATAAATCATCATGTCTCTCCATC 240
QY 81 AsnIysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
DB 241 AACAAAGAACTATGTTGACATGGACGAGTACCCCGTCACCCGAACTTCAGAACCGATGT 300
QY 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGly 120
DB 301 GTGAACATGATTGCACATCTATTCAATGCACCGTTAGAGGCGGAGACCGCGTCGGA 360
QY 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheIysArgIys 140
DB 361 GTAGGAACCGTTGGATCATCGAGGCCATAATGTTGGCCGTTTGGCCTTCAAGCGTAAA 420
QY 141 TrpGlnAsnLysAspGlyAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
DB 421 TGGCAGAAACGCGCAAGCTGAAGGCAACCCGTCGATAAACCCCAACATTGTCAACCGGA 480
QY 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
DB 481 GCCAATGTTCAAGTGTGGGAGAAATTCGCTAGGTACTTTGAGTTGAATTAAGGAA 540
QY 181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
DB 541 GTGAAATTGAGTGAAGGATACTATGTGATGGACCCCTCAACAAGCTGTGTATGTTGAT 600
QY 201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
DB 601 GAGAACACCAATTTGTTGGCGCCATTCTTGTTGCCACTCTTAATGGAGAAATCGAAGAT 660
QY 221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240
DB 661 GTTAAACTCTTGAACGATCTCTTGTCGAAAGAACAAAGAAACCGGATGGATACACCA 720
QY 241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
DB 721 ATCCACGTGGATGCGGCAAGTGGAGATTTCATTCACCGCTTTTGTATCCGGAATTGAA 780
QY 261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisIysTyrGlyLeu 280
DB 781 TGGGACTTTTAGACTTCCCTTGGTGAAGAGTATCAATGTGAGTGGTTCACAGTATGGACTT 840
QY 281 ValTyrAlaGlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300
DB 841 GTGTACGACGAGGATGTTGGTGTATCTGGAGAAACAAAGAGGATTTGCCTCAGGAACTC 900
QY 301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerIys 320
DB 901 ATCTTCCATATCAATTATCTTGGTCTGACCAACCCACTTTACTCTCAATTTCTCCAAA 960
QY 321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
DB 961 GGTTCAGTCAAGTCATGCTCAATACTACCAACTTATCCGATGGGCGCAGAGGTTTAC 1020
QY 341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
DB 1021 AGAANTGTATGGAGAAATTCAGAGAGATATGATCGTCCTAAGGGAAGGACTTGAGAG 1080
QY 361 ThrGluArgPheAsnIleValSerIysAspGluGlyValProLeuValAlaPheSerLeu 380
DB 1081 ACAGAAAGGTTCAACATCGTCTCAAAAGGACGAGGAGTGCCACTTGTCCCTTCTCCTTG 1140
QY 381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr 400

```
|||||
1141 AAAGATAGCAGCTGTACACTGAGTTCGAAATCCGACATGCTTCGAGTATGGATGG 1200
401 ILeValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgValVal 420
1201 ATAGTCCGCGCTACACAATGCTCCAAATGCACACACATCACTGTCTCTCGTGGTT 1260
421 ILeArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
1261 ATCAGAGAAGATTCTCGAGAACACTCGCTGAGAGACTTGTGATCGATATAGAGAAAGTG 1320
441 MetArgGluLeuAspGluLeuProSerArgValIleHisIysIleSerLeuGluGlnGlu 460
1321 ATGCGTGAGCTCGATGAGCTTCCTTCGAGAGTGATTCCAAAATATCATCTTGGACAAAG 1380
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1381 AAGAGTGAATCTAACACGATAAATCTGATGGTCACTGAGAGAGCGATATCGACNAG 1440
481 GlnArgAspIleIleThrGlyThrLysPheValAlaAspArgLysLysThrSerGly 500
1441 CAGAGATATCATCACTGGCTGGAGAGATTGTGCGCCACAGAGAGAGAGAGAGTGGT 1500
501 IleCys 502
1501 ATCTGC 1506

RESULT 3
AL43415
D D AAL43415 standard; cDNA; 1705 BP.
X X
C X AAL43415;
X X
T T 25-SEP-2002 (first entry)
X X Tobacco GAD1 coding sequence.
X X GAD; plant GABA production regulation; glutamic acid decarboxylase;
X X plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ss.
X X Nicotiana tabacum.
X X
H X Location/Qualifiers
T T 71..1561
T T /*tag= a
T T /product= "GAD1"
X X
X X WO200238736-A2.
X X 16-MAY-2002.
X X
X X 07-NOV-2001; 2001WO-US47447.
X X
X X 07-NOV-2000; 2000US-246367P.
X X (EMER-) EMERALD BIOAGRICULTURE CORP.
X X
X X Kinnersley AM, Turano FJ;
X X WPI; 2002-490073/52.
X X P-PSDB; AAO15137.
X X
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Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome

Claim 18; Page 56-57; 63pp; English.

The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a

CC polynucleotide encoding a functional plant glutamic acid decarboxylase
CC (GAD), to provide a transformed plant that expresses the GAD coding
CC sequence in response to a signal. Plants of this type have an enhanced
CC ability to tolerate environmental or other stresses. The present sequence
CC is the tobacco GAD1 coding sequence.
XX
SQ Sequence 1705 BP; 523 A; 301 C; 385 G; 496 T; 0 other;

Alignment Scores:
Pred. No.: 3,19e-223 Length: 1705
Score: 2240.00 Matches: 428
Percent Similarity: 92.05% Conservative: 35
Best Local Similarity: 85.03% Mismatches: 32
Query Match: 85.66% Indels: 8
DB: 24 Gaps: 3

US-10-006-852-2 (1-502) x AAL43415 (1-1705)

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QY 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
DB 71 ATGGTTCTGTCCAAAGACAGCGTCGAAAAGTGACGTCTCCATCCACTCCACTTCGCTTCC 130
QY 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
DB 131 CGATATGTTCTGACTTCTCTCCGAGGTTTAAAGTCCAGAGATTCCATACCAAGGAA 190
QY 41 AlaAlaTyrGlnIleIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
DB 191 GCAGCATATCAAAATCATAAATGATGAGCTTATGTTAGATGGAAATCCAAAGACTAAATTTA 250
QY 61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
DB 251 GCATCTTTTGTGACAAACATGGATGGAAACAGAGTGTAAACAACTGATGATGATTCAT 310
QY 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
DB 311 AACAGAAATTAGTTGACATGGATGGAATACCTGTAAACACTGAACTTCAGAAATCGATGT 370
QY 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
DB 371 GTAAACATGATAGCTCATTTGTTTAAACGACCACCTGGAGATGGAGAGACTGCACGTGA 430
QY 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
DB 431 GTTGAACCTGTGGATCTCTCTGAGGCTATTATGCTGTGCTGATAGCTTTTCAAGAGAAA 490
QY 141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
DB 491 TGGCAAAATTAATTAAGAGCCCAAGCGCCCTGTGACAGCCCAATATTGTCTACTGGT 550
QY 161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
DB 551 GCCAATGTCCAGTGTGTGGAGAAATTTGCAAGGTATTTTGAAGTGGAGCTAAAGGAA 610
QY 181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
DB 611 GTAAAGTTGAGTGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
QY 201 GluAsnThrIleCysValAlaAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
DB 671 GAGAACACAAATTTGTAGTGTCTATCTTGGTTCACACTCAATGTTGATTTGAGAGAT 730
QY 221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
DB 731 GTTAAAGCGCTTGAATGACCTCTTGATTTGAGAAGAACAAAGAAACCGGGTGGGACACTCA 790
QY 241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
DB 791 ATTCATGTGGATGACAGCAAGTGGTGATTTTATGACCAATCTCTTATCCAGAGCTTGA 850
QY 261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
DB 851 TGGGACTTTTAGATTGCCATTGGTGAAGAGATTAACCGTGAGTGGTGCACAAATATGCTTT 910
```



```
612 GTAAAGCTTAGTGAGGATGACTATGTCATGAGCCCTGAGAAAGCTGTGGAGATGGTGGAT 671
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
672 GAAACACCACTTTGTGTAGCTGCTATCTTAGTGTCCACCCTCAATGGAGAATTTGAAGAC 731
221 ValIleLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro 240
732 GTTAAGCGCTTGAATGATCTCTTGTGTCAGAGAACAAAGAAACCGGGTGGGACACTCCA 791
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
792 ATTCATGTGGATGCAGCAAGTGTGGTGGTATTATTCACCGTTCATTACCCAGAGCTTGAG 851
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
852 TGGGACTTTAGATTGCCATTAGTGAAGAGCATTAAATGTAAGTGGTCACAAATATGGTCTT 911
281 ValTyrAlaGlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuProGluGluLeu 300
912 GTCTATGCTGGTATTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 970
301 IlePheHisIleAsnTyrLeuGlyValAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
971 ATCTCCACATTAAATATCTTGGTGTGATCAACCTACTTCTCACTCAACTTTTCTAAA 1030
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
1031 GGTCTAGCCCAAGTAATGTCATAATATTACCACTTATTCGCTTGGTGTATGAGGGTTAC 1090
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
1091 AAGATGTGATGGAGAAATGTCAGAAAATGCATCGGTACTAAGAGAGGGCTAGAAAAG 1150
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
1151 ACAGGAAGATTCACATAATCTCCAGAAATTTGGAGTACCTTTAGTAGATTTCTCTCT 1210
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr 400
1211 AAAGACACAGGCAACACAGAGTTCGAGATTTCTGAAACTTTAAGCAGATTTGGTTGG 1270
401 IleValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgValVal 420
1271 ATTTCTCTGCATATATCTATGCCACCAACGCAACACACATTACAGTTCTCAGAGTTGTG 1330
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
1331 ATCAGAGAAGATTTCTCCGTCAGCTTTCGAGAGCAGCTGGTAAGAGACATCGAAAAGTC 1390
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
1391 CTTCATGAATCTGACACACATCCCTGACAGTGTCAATGCTAAGCTCGCTGTGGCCGAGGAG 1450
461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480
1451 CAGCGCGCTCGAATGCACGAGGTCAT-----AAGAAACAGATACGCGAAGTG 1501
481 GlnArgAspIleIleThrGlyTrpLysPheValAlaAsp---ArgLysLysThrSer 499
1502 CAGTTGGAGATGATACTGCATGGAGAAGTTGTTTGAAGAAAAGAAAGAAAGACTAAT 1561
500 GlyIleCys 502
1562 CGAGTTTGT 1570
RESULT 5
ID AAL43416
CD AAL43416 standard; cDNA; 1771 BP.
XX AAL43416
XX
XX
XX 25-SEP-2002 (first entry)
```

```
XX Tobacco GAD2 coding sequence.
DE
XX
XX GAD; plant GABA production regulation; glutamic acid decarboxylase;
KW plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ss.
XX
XX Nicotiana tabacum.
XX
XX Key Location/Qualifiers
CDS 67..1557
FT /*tag= a "GAD2"
FT /product= "GAD2"
XX
PN WO200238736-A2.
XX
XX 16-MAY-2002.
XX
XX 07-NOV-2001; 2001WO-US47447.
XX
XX 07-NOV-2000; 2000US-246367P.
XX
XX (EMER-) EMERALD BIOAGRICULTURE CORP.
XX
XX Kinnersley AM, Turano RJ;
XX
XX MPI; 2002-490073/52.
XX
XX P-PSDB; AAO15138.
XX
XX Making transformed plants that selectively increase gamma-aminobutyric
XX acid production, by incorporating a DNA construct with a polynucleotide
XX encoding a plant glutamic acid decarboxylase enzyme into plant's genome
XX
XX
XX Claim 18; Page 57; 63pp; English.
XX
XX The present invention relates to a method of producing a transformed
XX plant that selectively increases production of gamma-aminobutyric acid
XX (GABA) in response to a signal, by incorporating into the plant's genome
XX a DNA construct with a non-constitutive promoter operably linked to a
XX polynucleotide encoding a functional plant glutamic acid decarboxylase
XX (GAD), to provide a transformed plant that expresses the GAD coding
XX sequence in response to a signal. Plants of this type have an enhanced
XX ability to tolerate environmental or other stresses. The present sequence
XX is the tobacco GAD2 coding sequence.
XX
XX Sequence 1771 BP; 548 A; 295 C; 393 G; 535 T; 0 other;
```

```
Alignment Scores:
Pred. No.: 6,28e-219 Length: 1771
Score: 2199.00 Matches: 423
Percent Similarity: 90.85% Conservative: 34
Best Local Similarity: 84.10% Mismatches: 38
Query Match: 84.09% Indels: 8
DB: 24 Gaps: 3
US-10-006-852-2 (1-502) x AAL43416 (1-1771)
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QY 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db 67 ATGGTTCTGTCACACAGACAGCGTCGGAAGTAGTACGCTCCGTTCACTCCACCTTCGCTCC 126
QY 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
Db 127 CGATATGTTGCAACTTCTCTCCAGAGTTTAAATGCCAGAGAAATCAATACCAAGGAA 186
QY 41 AlaAlaTyrGlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
Db 187 GCAGCATATCAGATTATAAATGATGAGCTTATGTTAGATGAAATCCCAAGGCTAAATTTA 246
QY 61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
Db 247 GCATCTTTCGTTACCAATGATGGATGGAGCCAGAGATGTAATACGTTAATGATGATCCATT 306
```

```
81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
|||
307 AACAAAGAACTACGTTGATGGATGAATACCTGTACCACTGAGCTTCAGAAATCGATGT 366
|||
101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGly 120
|||
367 GTAATATGATAGCTCAATTTGTTTATGCACCACTGGAGATGGAGAGACTGCGATTGGA 426
|||
121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
|||
427 GTTGAAACTGTTGGATCCTCTGAAGCTATTATGCTTCTGGAATTAGCTTTTAAAGAGAAA 486
|||
141 TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
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487 TGGCAAAATAAATGAAAGCCCAAGGCAAGCCCTTTGATAAGCCCAATATTGTCAACGGT 546
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161 AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu 180
|||
547 GCTAATGTCCAGGTGTTGGAGAAATTTGCAAGGTATTTGAAGTGGAGTTGAAAGAA 606
|||
181 ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
|||
607 GTAAATTTGAGTGATGATACTATGTGATGACCTGAGAAAGCTGTGGAATTTGGTGGAT 666
|||
201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
|||
667 GAGAATACCAATTTGTGTGTCTATCTTAGTTCACACTCACTCAATGGTGAATTTGAAGAT 726
|||
221 ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro 240
|||
727 GTTAAGCGTTTGAATGACCTTTTGAATGAGAGAAACCAAGCCGGTGGACATCTCCA 786
|||
241 IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu 260
|||
787 ATTCAATGCGATGAGCAAGTGGTGGATTTATTGCACATTTCTTTTCCAGAGCTTGA 846
|||
261 TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu 280
|||
847 TGGGACTTTAGATTGCCATTGGAGAAAGATTAATGATGAGTGCACAAATATGTGCTT 906
|||
281 ValTyrAlaGlyIleGlyTyrValIleTyrArgAsnLysGluAspLeuProGluLeuLeu 300
|||
907 GTCTATGCTGATTTGTTGGCCATTTGGAGGATTAAGAGACTTGCCTGATGACTT 966
|||
301 IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys 320
|||
967 ATTTTCCACATCAATTAACCTTGGTGGTCTGATCAACTACTTCACTCTCAACTTCTTAAA 1026
|||
321 GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr 340
|||
1027 GGTTCCTAGCCCAAGTAATGCTCAATATTACCACTTATTCCTTGGTGGTGGTGGTTAC 1086
|||
341 ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys 360
|||
1087 AAGAATGTTATGGAGAAATTTGCAAGAAATATCAAGGTTATTAGAGAGAAATTTGAAAA 1146
|||
361 ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu 380
|||
1147 AGTGGAGATTTCAACATAATTCCTCAAGAAATTTGGAGTTCCTCTTAGTAGCAATTTCTCTT 1206
|||
381 LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTyr 400
|||
1207 AAGACACACGTCAACACAAATGAGTTGAAATTTCTGAACTCTTAGAAGATTGGATGG 1266
|||
401 IleValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgValVal 420
|||
1267 ATGTTCTTGGCATATACTATGCCACCAAAATGCTCAACATGTCACAGTTCTCAGAGTTGTC 1326
|||
421 IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal 440
|||
1327 ATTAGAGAAGATTTCTCCCGCACACTAGCGGAGCGACTGGTAAATAGACATTTGAAAAAGTC 1386
|||
441 MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu 460
|||
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Db 1387 TTCCACGGAGTAGACACACTTCCGGCGAGGTCAACGCTAAGCTAGCGGTG----- 1437

QY 461 LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys 480

Db 1438 ---GCCGAGGCGAATGGCAGCGCGTGCAT-----AAGAAAAACAGATAGAGAAGTG 1485

QY 481 GlnArgAspIleIleThrGlyTyrLysLysPheValAlaAsp---ArgLysLysThrSer 499

Db 1486 CAGCTAGAGATTACTACTGTCATGCTGTTGAAATTTTGCTGATAAGAGAGAAAGACTAAT 1545

QY 500 GlyIleCys 502

Db 1546 GGAGTTTGT 1554

RESULT 6

ID ABZ13132 standard; DNA; 1482 BP.

XX ABZ13132;

AC ABZ13132;

DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 937.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX WO200216655-A2.

PN 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

PF 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

DR Identifying a stress condition to which a plant cell has been exposed

PT and producing plants with increased tolerance to these abiotic stresses

PT

XX Claim 144; SEQ ID NO 937; 577pp + Sequence Listing; English.

PS The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides

CC in the plant cell with an array or probes representative of the plant

CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell

CC characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants

CC with increased tolerance to abiotic stress. The present sequence is that

CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used

CC in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed

CC specification but is based on sequence information supplied to Derwent by

CC the European Patent Office.

XX Sequence 1482 BP; 402 A; 331 C; 378 G; 371 T; 0 other;

SQ

Alignment Scores:

Pred. No.: 2,02e-212 Length: 1482

Score: 2135.50 Matches: 411

Percent Similarity: 88.78% Conservative: 32

est Local Similarity:	82.36%	Mismatches:	45
very Match:	81.66%	Indels:	11
B:	24	Gaps:	2
S-10-006-852-2 (1-502) x ABZ13132 (1-1482)			
y	1	MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer	20
b	1	ATGGTTTTGTCTAAGACAGATTCGGAATCTGATCTCTCAATCAATCAATCTTGTCTCT	60
y	21	ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu	40
b	61	CGTTACTCGCGCAACTCTCTCCAGATTGGAATGCTCGAAGCTCAATCCCAAGAA	120
y	41	AlaAlaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu	60
b	121	GCAGCTTACCAATCAATCAACGACGAGCTAATGCTCGATGTTAAACCAAGCTGAACCTA	180
y	61	AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle	80
b	181	GCTTCCTTCGTGACCAATGATGAGCCAGAAATGTGACAAGCTCATGATGGAGTCCATC	240
y	81	AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys	100
b	241	AACAGAACTACGTCGACATGGACGAGTACCTGTCACTAGCTTCGAAACCGATGT	300
y	101	ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly	120
b	301	GTTAAACATGATAGCACGCTCTTCAACGCGCGCTTGGTGACGCTGAAAGCTGCGTGTGT	360
y	121	ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys	140
b	361	GTTGCGACCGTCGATCGTCGAGCGCATATGATGTGCGCGGTGTGGCTTTTAAAGACAA	420
y	141	TrpGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly	160
b	421	TGGCAGAATAAGCGTAAGGCCRAAGGCTTCTTATGATAAGCCCAATATCGTAACCGGT	480
y	161	AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu	180
b	481	GCTAATGCTCCAGGTTTGTGGAGAAAATTCGCAAGGTATTTTCGAAGTGGAGCTTAAGGA	540
y	181	ValLysLeuSerGluGlyTyrTyrValMetAspProGlnAlaValAspMetValAsp	200
b	541	GTGAACCTTAGAGAAGACTATTACGTATGACCCCTGTAAAGCGCGTCGAAATGGTAGAC	600
y	201	GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp	220
b	601	GAATAACAAATTTGTGTGCTGCCATCCTCGGTTCAACGTTAACCGGTGAATTCGAAGAC	660
y	221	ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrAspThrPro	240
b	661	GTTAAGCTCTCTCAACGACCTCTTGTGAGAAAACCAAGCAAAACCGGATGGGACGCGCA	720
y	241	IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu	260
b	721	ATACAGTGGACGACGAGTGGTGGTTATTGCTCCGTTCTGTATCCGGAGCTGGAG	780
y	261	TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu	280
b	781	TGGGATTTCCGGCTACCGTTGGTTAAGAGTATTAAATGTGAGTGGTCACAAATACGGTTTG	840
y	281	ValTyrAlaGlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuProGluGluLeu	300
b	841	GTTTACGCCGGTATGTGTTGGTTGTATGGAGAACCAAAACCGGATTTGCTGATGAACCTT	900
y	301	IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys	320
b	901	ATCTTCCATATCAATATCTTGGCGCTGATCAACCAACCTTTACCTCAACTCTCCAAA	960
y	321	GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr	340
b	961	GGTTCAAGTCAAGTATTGCTCAGTACTACGAGCTGATTGCTTTGGATTGAGGGTTAT	1020
QY	341	ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys	360
Db	1021	CGCAATGTGATGGATAATTGTCGGGAAAAACATGATGGTACTAAGACAAGGATTAGAGAA	1080
QY	361	ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu	380
Db	1081	ACGGACCGCTTTTAAATCGTCTCCAAAGAAAACGGTGTTCGGTTAGTGGCGTTTCTCTC	1140
QY	381	LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTrp	400
Db	1141	AAAGATAGTAGCCGCCACACAGAGTTCGAGGTGGGCCCATACACTCCGTCGCTCGGCTGG	1200
QY	401	IleValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgValVal	420
Db	1201	ATCGTTCGGCGCTACACGATGCTCGGATCGCAGCATGCTCACTGTCTCTCGAGTTGTT	1260
QY	421	IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal	440
Db	1261	ATCCGAGAGAGATTTCTTCGAACCTTAGCCGAGAGATTGGTAGCTATTTCGAGAAGTT	1320
QY	441	MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu	460
Db	1321	CTACACGAGCTCGATACGCTTCGGCGAGGGTTCACGCCAAGATGGCTAATGGAAGATT	1380
QY	461	LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys	480
Db	1381	AACGGT-----GTTAAGAAGACGCCAGAGAGACG	1410
QY	481	GlnArgAspIleIleThrGlyTrpLysLysPheValAlaAspArgLysLysThrSer	499
Db	1411	CAGAGAGAGTCACGGCTACTGGAGAAGTTGTTG----GAGACTAAGAGACCAAC	1464
RESULT 7			
ID	AA143411	standard; cDNA; 1665 BP.	
XX	AA143411;		
AC	AA143411;		
XX	25-SEP-2002 (first entry)		
DT			
XX	A thaliana GAD2 coding sequence.		
DE			
XX	GAD; plant GABA production regulation; glutamic acid decarboxylase;		
KW	plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ss.		
XX	Arabidopsis thaliana.		
XX	Key Location/Qualifiers		
FT	17..1501		
FT	/tag= a		
FT	/product= "GAD2"		
XX	WO200238736-A2.		
PN			
XX	16-MAY-2002.		
PD			
XX	07-NOV-2001; 2001WO-US47447.		
PF			
XX	07-NOV-2000; 2000US-246367P.		
PR			
XX	(EMER-) EVERALD BIOAGRICULTURE CORP.		
PA			
XX	Kinnersley AM, Turano PJ;		
PI			
DR	WPI; 2002-490073/52.		
DR	P-PSDB; AAO15133.		
XX			
XX	Making transformed plants that selectively increase gamma-aminobutyric		
PT	acid production, by incorporating a DNA construct with a polynucleotide		
PT	encoding a plant glutamic acid decarboxylase enzyme into plant's genome		
XX			

S Claim 18; Page 53-54; 63pp; English.

X The present invention relates to a method of producing a transformed
C plant that selectively increases production of gamma-aminobutyric acid
C (GABA) in response to a signal, by incorporating into the plant's genome
C a DNA construct with a non-constitutive promoter operably linked to a
C polynucleotide encoding a functional plant glutamic acid decarboxylase
C (GAD), to provide a transformed plant that expresses the GAD coding
C sequence in response to a signal. Plants of this type have an enhanced
C ability to tolerate environmental or other stresses. The present sequence
C is the A. thaliana GAD2 coding sequence.

X Sequence 1665 BP; 490 A; 311 C; 423 G; 441 T; 0 other;

Alignment Scores:

red. No.: 8.88e-212 Length: 1665
core: 2130.00 Matches: 404
percent Similarity: 89.29% Conservatives: 46
est Local Similarity: 80.16% Mismatches: 42
very Match: 81.45% Indels: 12
B: 24 Gaps: 3

S-10-006-852-2 (1-502) x AAL43411 (1-1665)

Y	1	MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer	20
b	17	ATGGTTTGTGACAAACCCGCAACG---AATGATGAATCTGTCTGCACCATGTTCGGATCT	73
Y	21	ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu	40
b	74	CGTATGTCGCACACTACCTCCCAAGTATGAGATGGTGAGAAATCGATACCGAAAGAC	133
Y	41	AlaAlaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu	60
b	134	GCTGCATATCAGATCATAAAGATGAGCTGATGCTTATGCTTAACCCGAGGCTTAACCTA	193
Y	61	AlaSerPheValThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle	80
b	194	GCCTCGTTGTGACTACATGGATGGAACCGAGGTGACAAATCATCATGGAATCTATC	253
Y	81	AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys	100
b	254	AACAGAACTACGTTGATATGATGAGTACCTGTGCACACTGAGCTCCAGAACCGATGT	313
Y	101	ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAlaValGly	120
b	314	GTAACATATTAGCTGACTGTTCATATCGCCACTCGAGGAATCTGAGACGGCGTGGGA	373
Y	121	ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys	140
b	374	GTAGGGACAGTTGTTCTTCAGAAAGCCATCATGTTAGCCGGATTGGCTTCAAAGAA	433
Y	141	TrpGlnAsnLysArgLysAlaGluGlyIleProValAspLysProAsnIleValThrGly	160
b	434	TGGCAGAACAAACGCAAGGCTGAGGGTAAACCTTATGACAAACCCCAACATGTCTGGA	493
Y	161	AlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGluLeuLysGlu	180
b	494	GCCAAATGTTCAAGTTTCTCGGAGAAATTCGCTCGGTACTTCGAGGTGGAGCTAAAGGA	553
Y	181	ValLysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp	200
b	554	GTAACCTAAGTGAAGTTTACTACGTGATGGATCCAGACAGACGAGAAATGGTAGAC	613
Y	201	GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp	220
b	614	GAGAACCAATCTGTGTGCGAGCCATATTGGATCCACACTCAACGGTGAGTTCGAAGAC	673
Y	221	ValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTrpAspThrPro	240
b	674	GTGAACAGCTCTCAATGCTTGTCTAGTCAAGAAACAGGAGAGACTGGTTGGAACACCG	733
Y	241	IleHisValAspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGlu	260

Db	734	ATCCACGTGGATGCGACGAAGTGGAGGGTTTCATAGCTCCGTTTATCTATCTGAATTAGAA	793
Qy	261	TrpAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeu	280
Db	794	TGGACTTTAGACTTCTCTTGGTTAAGAGTATCAACGTGAGTGTCAAGTATGGACTG	853
Qy	281	ValTyrAlaGlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuProGluGluLeu	300
Db	854	GTCATGCTGTTGTTGGTCTGTGGAGGGCAGCAGAGGATTTGCCCTGAAGAGCTT	913
Qy	301	IlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsnPheSerLys	320
Db	914	ATCTTTCATATTAATTTATCTGGTGTGATCAACCCACTTTCACTCTCAATTTCTCAAG	973
Qy	321	GlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGluGlyTyr	340
Db	974	GGATCGAGCCAAATTTATGCTCAATACTACAGCTCATTCGCTCTGGATTCGAGGGGTAC	1033
Qy	341	ArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGlyLeuGluLys	360
Db	1034	AAAAATGTTGATCGGAATTCATAGAGAACATGGTGGTTCTCAAAGAAGGATAGAGAAA	1093
Qy	361	ThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAlaPheSerLeu	380
Db	1094	ACAGAGCCTTTCAACATAGTCTCAAGAGCACCAAGAGTGCAGTCTGCTCTCTCTC	1153
Qy	381	LysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArgTyrGlyTrp	400
Db	1154	AAGGACCATAGTTTCCACACAGAGTTCGAGATCTCTGAGATGCTACGTCGTTTGGCTGG	1213
Qy	401	IleValProAlaTyrThrMetProAsnAlaGlnHisIleThrValLeuArgValVal	420
Db	1214	ATCGTCCAGCTTACACTATGCTGCGATGCGATGCACAGCACATCAAGGTTCTCGGTGTC	1273
Qy	421	IleArgGluAspPheSerArgThrLeuAlaGluArgLeuValIleAspIleGluLysVal	440
Db	1274	ATCAGGAGAGATTTCTCAAGAACACTCGCGAGAGACTTGTGCTGATATTCGAAGTG	1333
Qy	441	MetArgGluLeuAspGluLeuProSerArgValIleHisLysIleSerLeuGlyGlnGlu	460
Db	1334	CTTCATGAGCTAGATACCTTGCCCTTCCAAGATATCTAAGAAGATGGGAATA-----	1384
Qy	461	LysSerGluSerAsnSerAspAsnLeuMetValThrValLysLysSerAspIleAspLys	480
Db	1385	-----GAAAGGATCGCGGAAATGTAAAGGAGAGAAAGATGGAGAG	1426
Qy	481	Gln-----ArgAspIleIleThrGlyTrpLysLysPheValAlaAspArgLysLysThr	498
Db	1427	GAGATCTGATGGAAGTTATTGTTGGATGGAGGAAGTTTGTGAAGGAGAGGAAGATG	1486
Qy	499	SerGlyIleCys 502	
Db	1487	AATGTTGTGTGC 1498	
RESULT 8			
AAQ74691			
ID	AAQ74691	standard; cDNA; 1783 BP.	
XX	AAQ74691;		
XX	25-MAR-2003	(updated)	
DT	22-JUN-1995	(first entry)	
XX	Early Ripening Tomato protein ERTD1 gene.		
XX	Early Ripening Tomato; transgenic plant; crop improvement;		
KW	fruit ripening; transformation; ss.		
XX	Lycopersicon esculentum.		
OS	WO9421794-A1.		
PN			
XX			


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b 1086 AAAATGGCGGTCGATATGCTCTAAGGATGTTGGGTTCTCTGTAGCATTTCT 1145
Y 380 LeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgTyrGly 399
b 1146 CTCAGGACAGACGCAATATACGGTATTTGAAGTATCTGAGCATCTCAGAAGATTGGA 1205
Y 400 TrpIleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeuArgVal 419
b 1206 TGGATCGTCCTCATACACAATGACCACCGGATGCTGAACACATTCCTGACTGCGGGTT 1265
Y 420 ValIleArgGluAspPheSerArgTyrThrLeuAlaGluArgLeuValIleAspIleGluLys 439
b 1266 GTCAATAGAGGATTTCAGCCACACAGCTAGCTGAGAGACTGTGTTCTGACATTGAGAAA 1325
Y 440 ValMetArgGluLeuAspGluLeuProSerArgValIleHisLysIle-----SerLeu 457
b 1326 ATTCTGTGAGAGTTGGACACACAGCTCTCTGTTGCCACCAAGCTTCGCTGTCACCT 1385
Y 458 GlyGlnGluLysSerGluSerAsnSerAspAsnLeu-----MetValThrVal 473
b 1386 GCTGAGGAGACTGCGTGATGATCAACAGGGGTGATGGGCTTCATCATTTTCACATGGATACTGTA 1445
Y 474 LysLysSerAspIleAspLysGlnArgAspIleIleThrGlyTrpLysLysPheValAla 493
b 1446 -----GAGACTCAGAAGACATTATCAAACTTGGAGAAATCGCAGGG 1490
Y 494 AspArgLysLysThrSerGlyIleCys 502
b 1491 -----AAGAAGACCGGAGCTGC 1511

RESULT 10
AAC36324
AAC36324 standard; DNA; 1605 BP.
AAC36324;
X C X C X C X
T 17-OCT-2000 (first entry)
E Arabidopsis thaliana DNA fragment SEQ ID NO: 13376.
X X X X X X X
W Hybridisation assay; genetic mapping; gene expression control;
W protein identification; signal transduction pathway;
W metabolic pathway; promoter; termination sequence; ss.
X Arabidopsis thaliana.
X EP1033405-A2.
D 06-SEP-2000.
X 25-FEB-2000; 2000EP-0301439.
X 25-FEB-1999; 99US-0121825.
R 03-MAR-1999; 99US-0123180.
R 09-MAR-1999; 99US-0123548.
R 23-MAR-1999; 99US-0125788.
R 25-MAR-1999; 99US-0126264.
R 29-MAR-1999; 99US-0126785.
R 01-APR-1999; 99US-0127462.
R 06-APR-1999; 99US-0128214.
R 08-APR-1999; 99US-0128714.
R 16-APR-1999; 99US-0129845.
R 19-APR-1999; 99US-0130077.
R 21-APR-1999; 99US-0130449.
R 23-APR-1999; 99US-0130510.
R 23-APR-1999; 99US-0130891.
R 28-APR-1999; 99US-0131449.
R 30-APR-1999; 99US-0132048.
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R 04-MAY-1999; 99US-0132484.
R 05-MAY-1999; 99US-0132485.
R 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
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PR 01-JUN-1999; 99US-0137222.
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PR 15-JUL-1999; 99US-0144005.
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PR 16-JUL-1999; 99US-0144086.
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PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
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PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
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22-JUL-1999; 99US-0145192.
23-JUL-1999; 99US-0145145.
23-JUL-1999; 99US-0145218.
23-JUL-1999; 99US-0145224.
26-JUL-1999; 99US-0145276.
27-JUL-1999; 99US-0145913.
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27-JUL-1999; 99US-0145919.
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03-AUG-1999; 99US-0147038.
04-AUG-1999; 99US-0147204.
04-AUG-1999; 99US-0147302.
05-AUG-1999; 99US-0147192.
05-AUG-1999; 99US-0147260.
06-AUG-1999; 99US-0147303.
06-AUG-1999; 99US-0147416.
09-AUG-1999; 99US-0147493.
09-AUG-1999; 99US-0147935.
10-AUG-1999; 99US-0148171.
11-AUG-1999; 99US-0148319.
12-AUG-1999; 99US-0148341.
13-AUG-1999; 99US-0148565.
13-AUG-1999; 99US-0148684.
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17-AUG-1999; 99US-0149175.
18-AUG-1999; 99US-0149426.
20-AUG-1999; 99US-0149722.
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23-AUG-1999; 99US-0149902.
23-AUG-1999; 99US-0149930.
25-AUG-1999; 99US-0150566.
26-AUG-1999; 99US-0150884.
27-AUG-1999; 99US-0151065.
27-AUG-1999; 99US-0151066.
27-AUG-1999; 99US-0151080.
30-AUG-1999; 99US-0151303.
31-AUG-1999; 99US-0151438.
01-SEP-1999; 99US-0151930.
07-SEP-1999; 99US-0152363.
10-SEP-1999; 99US-0153070.
13-SEP-1999; 99US-0153758.
15-SEP-1999; 99US-0154018.
16-SEP-1999; 99US-0154039.
20-SEP-1999; 99US-0154779.
22-SEP-1999; 99US-0155139.
23-SEP-1999; 99US-0155486.
24-SEP-1999; 99US-0155859.
28-SEP-1999; 99US-0156458.
29-SEP-1999; 99US-0156596.
04-OCT-1999; 99US-0157117.
05-OCT-1999; 99US-0157753.
06-OCT-1999; 99US-0157865.
07-OCT-1999; 99US-0158029.
08-OCT-1999; 99US-0158232.
12-OCT-1999; 99US-0158369.
13-OCT-1999; 99US-0159293.
13-OCT-1999; 99US-0159294.
13-OCT-1999; 99US-0159295.
14-OCT-1999; 99US-0159329.
14-OCT-1999; 99US-0159330.
14-OCT-1999; 99US-0159331.
14-OCT-1999; 99US-0159637.
14-OCT-1999; 99US-0159638.
18-OCT-1999; 99US-0159584.
21-OCT-1999; 99US-0160741.
21-OCT-1999; 99US-0160767.
21-OCT-1999; 99US-0160768.
21-OCT-1999; 99US-0160770.
21-OCT-1999; 99US-0160814.

21-OCT-1999; 99US-0160815.
22-OCT-1999; 99US-0160980.
22-OCT-1999; 99US-0160981.
22-OCT-1999; 99US-0160989.
25-OCT-1999; 99US-0161404.
25-OCT-1999; 99US-0161405.
25-OCT-1999; 99US-0161406.
25-OCT-1999; 99US-0161359.
26-OCT-1999; 99US-0161360.
26-OCT-1999; 99US-0161361.
28-OCT-1999; 99US-0161920.
28-OCT-1999; 99US-0161992.
28-OCT-1999; 99US-0161993.
29-OCT-1999; 99US-0162142.
Alignment Scores:
Pred. No.: 1,3e-194 Length: 1605
Score: 1965.00 Matches: 372
Percent Similarity: 86.29% Conservative: 56
Best Local Similarity: 75.00% Mismatches: 62
Query Match: 75.14% Indels: 6
DB: 21 Gaps: 3
US-10-006-852-2 (1-502) x AAC36324 (1-1605)
QY 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
DB 40 ATGGTACTCGCA--ACCACTCTGACTCCGACGAGCATTTGGCATTTCCACTTTTGGCTTCT 96
QY 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40
DB 97 AGATATGTCGGTGGTGTTCACAGGTTCAAGATGCTGACCATTCGATGCCAAGAT 156
QY 41 AlaIaTyrGlnIleLeuAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
DB 157 GCTGCTTATCAAGTATCATGATGATGATGCTTGTGATGATTAATCCAGGCTTAACCTA 216
QY 61 AlaSerPheValThrThrTriMetGluProGluCysAspLysLeuIleMetSerSerIle 80
DB 217 GCCTCCTTTGTACACACTTGGATGGAACCTGAGTGTGACAACTCATCATGATTTCTGTC 276
QY 81 AsnLysAsnTyrValAspMetAspGluTyrProValThrGluLeuGlnAsnArgCys 100
DB 277 AATAAGAACTATGTTGATATGATGATGAATATCCTGTCCACTGAGCTCCAGAACGGTGT 336
QY 101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGlnAlaGluThrAlaValGly 120
DB 337 GTAAATATGATAGCAAACTTTTCCATGCTCCCGTTGGAGAAAGACGAGGCTGCTATTGGG 396
QY 121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
DB 397 TGTGGAAGCTGTGGTTCACTGAGGCTATAATGCTGTGCTTTGGCTTTTCAAAAGGAAA 456
QY 141 TrpGlnAsnLysAsgLysAlaGluGlyLysProValAspLysProAsnIleValThrGly 160
DB 457 TGGCAACATAGAGAGAAAGCTCAGGGTCTACTTATGATAAGCCTAACATTTGTCACCTGA 516
QY 161 AlaAsnValGlnValCysTyrPglulysPheAlaArgTyrPheGluValGluLeuLysGlu 180
DB 517 GCCAATGTTCAAGTGTGCTGGAGAAAGTTTCAAGAGTACTTTGAGGTAGAGCTCAAGAG 576
QY 181 VallysLeuSerGluGlyTyrTyrValMetAspProGlnGlnAlaValAspMetValAsp 200
DB 577 GTGAAACTAAGTGAAGACTACTATGTTATGATCCAGCTAAAGCTGTAGAGATGGTGGAT 636
QY 201 GluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAsp 220
DB 637 GAGATACCATCTGTGTTGCAGCAATTCAGATCTACACTTACTGAGAGATTTGAGGAC 696
QY 221 VallysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyrPheAspThrPro 240
DB 697 GTTAAGCAATTGAACGATCTCTTAGCTGAGAAAAACGACAGACAGGATGGGAAACTCCT 756

PR	07-NOV-2000; 2000US-246367P.
XX	(EMER-) EMERALD BIOAGRICULTURE CORP.
PA	
XX	
PI	Kinnersley AM, Turano FJ;
XX	
DR	WPI; 2002-490073/52.
DR	P-PSDB; AAOL5135.
XX	
XX	Making transformed plants that selectively increase gamma-aminobutyric
PT	acid production, by incorporating a DNA construct with a polynucleotide
PT	encoding a plant glutamic acid decarboxylase enzyme into plant's genome
PT	-
XX	
PS	Claim 18; Page 55; 63pp; English.
XX	
CC	The present invention relates to a method of producing a transformed
CC	plant that selectively increases production of gamma-aminobutyric acid
CC	(GABA) in response to a signal, by incorporating into the plant's genome
CC	a DNA construct with a non-constitutive promoter operably linked to a
CC	polynucleotide encoding a functional plant glutamic acid decarboxylase
CC	(GAD), to provide a transformed plant that expresses the GAD coding
CC	sequence in response to a signal. Plants of this type have an enhanced
CC	ability to tolerate environmental or other stresses. The present sequence
CC	is the A. thaliana GAD4 coding sequence.
XX	
SQ	Sequence 2121 BP; 626 A; 412 C; 473 G; 610 T; 0 other;
Alignment Scores:	
Pred. No.:	1.8e-191 Length: 2121
Score:	1936.50 Matches: 410
Percent Similarity:	61.99% Conservative: 32
Best Local Similarity:	57.50% Mismatches: 46
Query Match:	74.05% Indels: 226
DB:	24 Gaps: 7
US-10-006-852-2 (1-502) x AAL43413 (1-2121)	
Qy	1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
Db	1 ATGTTTGTCTTAAGACAGTTTCCGATCTGATGTCATTCATTCATTCACATTTGCTTCT 60
Qy	21 ArgTyrValArgThrSerLeuPro----- 28
Db	61 CGTTAGTCGCGCAACTCTCTTCCACGGTAAACAACCTGTGTAAACAAATCTTTTGTCTAATG 120
Qy	28 ----- 28
Db	121 TTTTCGTCAACAATAGTACATGATGATGAATCAACCTTGGATAGTTTTTTTTTGGCGG 180
Qy	28 ----- 28
Db	181 TGGTTAATGTTGTAGATTATTATGTGTTATATACTATAAGGAAGGACATGTTTCGTATT 240
Qy	29 -----ArgPheLysMetProGluAsnSerIlePro 38
Db	241 TTTAACTTAATGTATCATCATTTTCATCATATTAGATTCGAAATGCTGAGAACTCAATCCCA 300
Qy	39 LysGluAlaAlaTyrGlnIleAlaAsnAspGluLeuMetLeuAspGlyAsnProArgLeu 58
Db	301 AARGAGAGAGCTTACCNAATCATCAACGACGAGCTAATGCTCGATGTTAACCCCAAGCTG 360
Qy	59 AsnLeuAlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSer 78
Db	361 AACCTAGCTTCCTTCGTACCACATGGATGGAGCGCAGAAATGTGCACAGCTCATGATGGAG 420
Qy	79 SerIleAsnLysAsnTyrValAsnMetAspGluTyrProValThrThrGluLeuGlnAsn 98
Db	421 TCCATCAACAAGAACTAGCTGCATGACGACGAGTACCCTGTCCACTGAGCTTCAGAAC 480
Qy	99 ArgCysValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThrAla 118
Db	481 CGATGTTTAAATATATAGACAGCTCTCTTCAACGCGCGCTTGTGTGACGTGAGCTGCC 540

119 ValGlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLys 138
 541 GTTGGTGTGGACCGTCGATCGTCGGAGCGAATATATGTTGGCGGTTTGGCTTTTAAAG 600
 139 ArgLysTyrGlnAsnLysArgLysAlaGluGlyLysProValAspLysProAsnIleVal 158
 601 AGACAATGCCAGATAAGCGTAAGGCCCAAGGGCTTCCTTATGATAAGCCCAATATCGTA 660
 159 ThrGlyAlaAsnVal----- 163
 661 ACCGGTCTAATGTCCAGGTAAACCAAAACAAAATTCATGAATATTAACCAAGACAAA 720
 164 -----GlnVa 165
 721 ATTGAATTTATCAATCCGGTTAAGTTATATGTGACTCAATTTCCGGTTCAATACAGGT 780
 165 lCysTrpGluLysPheAlaArgTyrPheGluValGluLysGluValLysLeuSerG1 185
 781 TTGCTGGGAGAAATTCGCAAGGTATTTCCGAAGTGAGCTTAAGGAAGTGAACCTTAAGAGA 840
 185 uGlyTyrTyrValMetAspProGlnAlaValAspMetValAspGluAsnThrIleCy 205
 841 AGACTATTACGTGATGGACCTGTAAAGCGGTGAAATGGTAGACGAAACACAAATTTG 900
 205 sValAlaAspIleLeuGlySerThrLeuAsnGlyGluPheGluAspValLysLeuLeuAs 225
 901 TGTCTGCTGCATCTCGGTTCACCGTTAACCGTTGAATTCGAAGACGTTAAGCTCTCTCAA 960
 225 nAspLeuLeuValGluLysAsnLysGluThrGly----- 236
 961 CGACCTCTTGTGAGAAAAACAAGCAACCGG- GTAATTAACCAACCAACCGAGAAACAAG 1019
 236 ----- 236
 1020 CTAATATCGATTGTAATCGGTTGGAGTCGGTTTTAACGTTCTAAACACAAATTTGCAG 1079
 237 -TrpAspThrProIleHisValAspAlaSerGlyGlyPheIleAlaProPheLeuTy 256
 1080 ATGGGACACGCCAATACACGTGACGACGAGAGTGGTGGGTTTATGCTCCGTTCTTGTA 1139
 256 rProGluLeuGluTyrAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHi 276
 1140 TCCGGAGCTGGAGTGGGATTCGCGTACCGTTGGTTAAGATATTAATGTAGTGGTCA 1199
 276 sLysTyrGlyLeuValTyrAlaGlyIleGlyTyrValIleTyrAsnLysGluAspLe 296
 1200 CAAATACGGTTTGGTTTACCGCGTATTGGTTGGTTGTATCGAGAACCAACCGAATTT 1259
 296 uProGluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrIle 316
 1260 GCCTGATGAACCTATCTCCATATCAATTTATCTTGGCGTGTATCAACCAACCTTTACACT 1319
 316 uAsnPheSerLys----- 320
 1320 CAACCTCTCCAAAGGTACATTACCATAAGTCCATACATATATACTTCAATATATTT 1379
 321 -----Glyse 322
 1380 TTGGTGTATGGAATGTTTTATAGACTAAACATTGTGATAATGCTGTATAAACCAAGGTTTC 1439
 322 rSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHisGlu----- 338
 1440 AAGTCAAGTGATGCTCAGTACTACCAGCTGATTCGTTCTGGATTTCGAGGTAATAATAA 1499
 338 ----- 338
 1500 CTCAAAATAGCAATATATTACCAATGGTCAATAAAGAAACTAGATGTATATATTATTA 1559
 338 ----- 338
 1560 AGTTGTTACTTGTACTATACTTTGAAATTAAGCGTTCCTTAACATGACTAGTTTGGTATT 1619

339 -----GlyTyrArgAsnValMetGluAsnCy 347
 1620 GTGTAATTAATAATGTTTTCTTGTGTTAGGTTATCGCAATGTGATGATAATTG 1679
 347 sArgGluAsnMetIleValLeuArgGluGlyLeuGluLysThrGluArgPheAsnIleVa 367
 1680 TCGGGAAACATCATGATGTTACTAAGAACAAGATTAGAGAAAACGGGACGTTTTAAAAATCGT 1739
 367 lSerLysAspGluGlyValProLeuValAlaPheSerLeuLysAspSerSerCysHisTh 387
 1740 CTCCAAGAAAACGGTTTCCTGTAGTGGGTTTTCTCTCAAGATAGTAGCCGCCACAA 1799
 387 rGluPheGluIleSerAspMetLeuArgTyrGlyTyrIleValProAlaTyrThrMe 407
 1800 CGAGTTTCGAGTGGCCCATACATCCGTCGCTTCGGCTGGATCGTTCCTCCGCTTACACGAT 1859
 407 tProProAsnAlaGlnHisIleThrValLeuArgValValIleArgGluAspPheSerAr 427
 1860 GCCTGCGATGCCAGCAIGTCACGTCTTCGAGTTGTATCCGAGAAATTTCTCTCG 1919
 427 gThrLeuAlaGluArgLeuValIleAspIleGluLysValMetArgGluLeuAspGluLe 447
 1920 AACCTTAGCCGAGAGATTGGTAGCTGATTCGAGAAAGTTCTACACGAGCTCGATACGCT 1979
 447 uProSerArgValIleHisLysIleSerLeuGlyGlnGluLysSerGluSerAsnSerAs 467
 1980 TCCGGCGAGGGTTTCACGCCAAGATGGCTAATGAAAAGTTAACCGGT----- 2025
 467 pAsnLeuMetValThrValLysLysSerAspIleAspLysGlnArgAspIleIleThrG1 487
 2026 -----GTTAAGAAAGCCGACAGAGAGACGACAGAGAGAGTACGGCCTA 2069
 487 YTrpLysLysPheValAlaAspArgLysLysThrSer 499
 2070 CTGGAAGAAGTTGTG--GAGACTAAGAAGACCAAC 2103

RESULT 12
 AA170004
 ID AA170004 standard; DNA; 1180 BP.
 XX
 AC AA170004;
 XX
 DT 24-JAN-2002 (first entry)
 XX
 DE Tomato glutamate decarboxylase clone T-gad-19 DNA sequence.
 XX
 KW Tomato; glutamate decarboxylase; GAD; transgenic plant; T-gad-19; ds.
 XX
 OS Lycopersicon esculentum.
 XX
 FN JP2001238555-A.
 XX
 PD 04-SEP-2001.
 XX
 PF 13-DEC-2000; 2000JP-0404172.
 XX
 PR 13-DEC-1999; 99JP-0352552.
 XX
 PA (AJIN) AJINOMOTO KK.
 XX
 DR WPI; 2001-610050/70.
 XX
 PT Creation of a transgenic plant of improved amino acid composition,
 XX involves transformation with antisense sequences -
 PS Example 1; Page 13-14; 18pp; Japanese.
 XX
 CC The present invention relates to a method for creating a transgenic plant
 CC which accumulates a larger amount of at least one amino acid of edible
 CC part than a natural plant of the same species cultured under a same
 CC condition. The method involves transforming a plant with a genetic
 CC structure containing an antisense sequence of a gene sequence encoding
 CC glutamate decarboxylase (GAD) and a controlling sequence which can

C express the antisense sequence. The resultant transgenic plant has high
 C added value. The present sequence is the DNA sequence for clone T-gad-19
 C of the tomato GAD gene, which was used to illustrate the present
 C invention.

X Q Sequence 1180 BP; 372 A; 188 C; 276 G; 344 T; 0 other;

Alignment Scores:

red. No.: 2,32e-181 Length: 1180
 core: 1836.00 Matches: 347
 Percent Similarity: 94.40% Conservativeness: 24
 est Local Similarity: 88.30% Mismatchatches: 22
 Query Match: 70.21% Indels: 1
 B: 22 Gaps: 0

IS-10-006-852-2 (1-502) x AAI70004 (1-1180)

Y 38 ProLysGluAlaAlaTyrGlnIleAAsnAspGluLeuMetLeuAspGlyAsnProArg 57
 b 1 CCAAGGAAGCAGCATATCAGATTCTAAATGATGAACCTTATGTAGTGAATCCAAAGG 60
 Y 58 LeuAsnLeuAlaSerPheValThrThrTyrMetGluProGluCysAspLysLeuIleMet 77
 b 61 TTGAATTGGCATCTTTTGTGACACATGGATGGAACCAAGATGTGACAAATTTGATGATG 120
 Y 78 SerSerIleAsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGln 97
 b 121 GATTCATTAACAAAATTTATGTTGACATGATGAATATCTCTGACCACTGAGCTTCAG 180
 Y 98 AsnArgCysValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluAlaGluThr 117
 b 181 AATCGGTGTGTAACATGATGAGCCATTTATTTAATGCACCCTTGAAGATGAGAAACT 240
 Y 118 AlaValGlyValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPhe 137
 b 241 GCAGTTGGAGTTGGAACAGTTGGTTCTTCAGAGCCATTATGCTTGCTGATTTGGCCTTT 300
 Y 138 LysArgLysTrpGlnAsnLysArgGlyAlaGluClyLysProValAspLysProAsnIle 157
 b 301 AAGAGAAATGGCAAAACAAATGAAAGCCCAAGAAAGCCCTATGATTAAGCCCAACATT 360
 Y 158 ValThrGlyAlaAsnValGlnValCysTrpGluLysPheAlaArgTyrPheGluValGlu 177
 b 361 GTTACTGGTGCTAATGTCAGGTGTGGGAAAAATTTGCAAGGTATTTTGAAGTTGAG 420
 Y 178 LeuLysGluValLysLeuSerGluClyTyrTyrValMetAspProGlnGlnAlaValAsp 197
 b 421 CTNAAAGAAAGTGAAGTTGACTGATGATGATCTATGATGAGCCCTGAGAAAGCTGTGGAA 480
 Y 198 MetValAspGluAsnThrIleCysValAlaAspIleLeuGlySerThrLeuAsnGlyGlu 217
 b 481 ATGGTTGATGAGAACACAAATTTGTAGTCTCTATTTTGGGTTCACCTCGAATGGGGAG 540
 Y 218 PheGluAspValLysLeuLeuAsnAspLeuValGluLysAsnLysGluThrGlyTyr 237
 b 541 TTTGAGGAAGTGAAGAAATTTGAATGACCTCTCTATT-GAAAAGAACAGGAACAGGGTGG 599
 Y 238 AspThrProIleHisValAspAlaAspSerGlyPheIleAlaProPheLeuTyrPro 257
 b 600 GACACTCCAATTCATGTGGATGCAGCTAGTGGTGGATTATTTGCACCATTATATATCCA 659
 Y 258 GluLeuGluTyrAspPheArgLeuProLeuValLysSerIleAsnValSerGlyHisLys 277
 b 660 GAACCTTGATGGACCTTTAGATTGGCATATTGTTAAAGATATAATGTCAGCGGTCAAG 719
 Y 278 TyrGlyLeuValTyrAlaGlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuPro 297
 b 720 TATGGCTTGTATATGCTGGTGTGGTGGTTCATATGCGGAGCAAGGAGACTTGCCTCC 779
 Y 298 GluGluLeuIlePheHisIleAsnTyrLeuGlyAlaAspGlnProThrPheThrLeuAsn 317
 b 780 GATGAACCTTATTTTTCATATTAAATTACCTTGGGTCTGATCAACCTTACTTTTCCACCTCAAT 839

QY 318 PheSerLysGlySerSerGlnValIleAlaGlnTyrTyrGlnLeuIleArgLeuGlyHis 337
 Db 840 TTCCTAAAGGATCAAGTCAAGTAATTTGCTCAATATTATCAACTAATTCGTTTGGTTAT 899
 QY 338 GluGlyTyrArgAsnValMetGluAsnCysArgGluAsnMetIleValLeuArgGluGly 357
 Db 900 GAGGGTTATAAGAACGTCATGAAGATTTGCTTATCAAAACGCAAGGGTACTAAACAGAGGA 959
 QY 358 LeuGluLysThrGluArgPheAsnIleValSerLysAspGluGlyValProLeuValAla 377
 Db 960 ATCACAATAATGGGAAGATTCGAGATTGTCTCCAAAGGATTTGGTGTTCCTTGGTTGCA 1019
 QY 378 PheSerLeuLysAspSerSerCysHisThrGluPheGluIleSerAspMetLeuArgArg 397
 Db 1020 TTTTCTCTTAAAGACAATAGCAAAACATGATGAGTTTGAAGTATCTGAACCTTTAAAGGAGA 1079
 QY 398 TyrGlyTyrIleValProAlaTyrThrMetProProAsnAlaGlnHisIleThrValLeu 417
 Db 1080 TTTGGATGGATTGTTCCAGCATACACATATGCCAGATGCTCAACACATCACAGTTCTT 1139
 QY 418 ArgValValIleArgGluAspPheSerArgThrLeuAla 430
 Db 1140 AGAGTTGTTATTAGAGAAGATTTCTCCGTACACTCGCC 1178
 RESULT 13
 AAL43412
 ID AAL43412 standard; DNA; 2493 BP.
 XX
 AC AAL43412;
 DT 25-SEP-2002 (first entry)
 XX
 DE A thaliana GAD3 coding sequence.
 XX
 KW GAD; plant GABA production regulation; glutamic acid decarboxylase;
 KW plant stress; GABA; gamma-aminobutyric acid; stress resistance; gene; ds.
 XX
 OS Arabidopsis thaliana.
 XX
 FN WO200238736-A2.
 XX
 PD 16-MAY-2002.
 XX
 PF 07-NOV-2001; 2001WO-US47447.
 XX
 PR 07-NOV-2000; 2000US-246367P.
 XX
 PA (EMER-) EMERALD BIOAGRICULTURE CORP.
 XX
 PI Kimmersley AM, Turano FU;
 XX
 DR WPI; 2002-490073/52.
 XX
 DR P-PSDB; AAO15134.
 XX
 PT Making transformed plants that selectively increase gamma-aminobutyric
 PT acid production, by incorporating a DNA construct with a polynucleotide
 PT encoding a plant glutamic acid decarboxylase enzyme into plant's genome
 PT
 XX
 PS Claim 18; Page 54-55; 63pp; English.
 XX
 CC The present invention relates to a method of producing a transformed
 CC plant that selectively increases production of gamma-aminobutyric acid
 CC (GABA) in response to a signal, by incorporating into the plant's genome
 CC a DNA construct with a non-constitutive promoter operably linked to a
 CC polynucleotide encoding a functional plant glutamic acid decarboxylase
 CC (GAD), to provide a transformed plant that expresses the GAD coding
 CC sequence in response to a signal. Plants of this type have an enhanced
 CC ability to tolerate environmental or other stresses. The present sequence
 CC is the A. thaliana GAD3 coding sequence.
 XX
 SQ Sequence 2493 BP; 783 A; 458 C; 507 G; 745 T; 0 other;

Alignment Scores:

```

Seq1: 9.54e-181 Length: 2493
Core: 1834.50 Matches: 395
Similarity: 52.76% Conservative: 44
Local Similarity: 47.48% Mismatches: 52
Query Match: 70.15% Indels: 342
B: 24 Gaps: 6

S-S-10-006-852-2 (1-502) x AAL43412 (1-2493)
1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20
|||||
1 AUGGTTTATCTAAGACAGCTTCCAAATCCGATGATTCATTCATTCATTCCTCC 60
21 ArgTyrValArgThrSerLeuPro-----28
|||||
61 CGTTATGTCGGCAACTCTATCTC-ACGGTAAGAAGTTGAACACACATTTATTTTGTGTTA 119
28 -----28
120 ATGTTTTCATTGGTAAGTCTCTAAAACTTAGCCTAGACGACGATACACAGCATCTT 179
28 -----28
180 GATCTAGATTCAATATTTATTACAGAAATATTTATTTTATATACGATATAGTTCMG 239
28 -----28
240 ATTTTAAATTTTGGGTACATAGAGAAATACTAGATTCTAACGAAATTAACCACTTGCA 299
28 -----28
300 CTGAAGATCCGAGCATAAAGTGTTACTATATATAAGAGTATTTTCTTTTAAATCTTA 359
29 -----ArgPheLysMetProGluAsnSerIleProLysGlu 40
360 AGCTAAATATCAATTTTTCATCAGATTTCGAAATACCTTAGAATCTCGATCCCTAAGNA 419
41 AlaAlaTyrGlnIleAsnAspGluLeuMetLeuAspGlyAsnProArgLeuAsnLeu 60
420 GCAGCATACCAATCATCAACGACGAGCTCAAGTTTGACGGTAACCCGAGGCTAAACCTG 479
61 AlaSerPheValThrThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
480 GCCTCCTTTGTGCCACTTGGATGGAGCGAGATGTGACAGCTCATGATGGAATCCATC 539
81 AsnLysAsnTyrValAspMetAspGluTyrProValThrThrGluLeuGlnAsnArgCys 100
540 AACAGAAACAACGTTGAGATGGACCATACCTCTGTTACCCGACCTTCAGATCGATGC 599
101 ValAsnMetIleAlaHisLeuPheAsnAlaProLeuGluGluAlaGluThrAlaValGly 120
600 GTTAACATGATTGCGGCTCTCTTCAACGGCGCTTTTAGTGAAGGTGAAGCGCCATTGGT 659
121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
660 GTTGGCACGCTGGGGTCATCGAGGCGAGTGTGGCCGAGCTGGCCCTTTAAGACAG 719
141 TrpGlnAsnLysArgLysAlaGluLysLysProValAspLysProAsnIleValThrGly 160
720 TGGCAGACAAGCGTAAGCCCTTAGGCTGCTTATGATAGACCTTAATATTGTACCGGA 779
161 AlaAsn-----162
780 GCCAATATTTCAGGTAAACCAAAATTTGATTAATTTTAAACCGGTTTAGGTCTAT 839
163 -----ValGlnValCysTrpGluLysPheAlaArgTyr 173
840 GTTTACATTGACTCAATTTCCGGTTCAATACAGGTTTGGTTGGAGAAATTTGCAAGGTAT 899
174 PheGluValGluLeuLysGluValLysLeuSerGluGlyTyrTyrValMetAspProGln 193
900 TTTGAAGTGGAGCTTAAGAGTGAAGCTGAGAGAGGATATTACGTTGATGACCCCTGAC 959
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QY 194 GlnAlaValAspMetValAspGluAsnThrIleCysValAlaAspIleLeuGlySerThr 213
Db 960 AAGCGGTTGAATGGTAGAGCAAAACACATATATGCGTCGTGGCCATCCTCGGTTCGACA 1019
QY 214 LeuAsnGlyGluPheGluAspValLysLeuLeuAsnAspLeuLeuValGluLysAsnLys 233
Db 1020 CTAACCGGAGAAATTCGAAGACGTTAAGCTCCTCAACGACCTTTTAGTCGAGAAAAACAAG 1079
QY 234 GluThrGly-----236
Db 1080 AAAACCGGTAATTTGAATCAAAACCACTAAACAATTAATTTTATATACTTTTCCTCTAGA 1139
QY 236 -----236
Db 1140 AATATTACAATTTCTAACGTCGAGATATATTTGCTTAGAAAAATATTTTATTTTTCGAATGAA 1199
QY 236 -----236
Db 1200 TATAAACTTATTAAACCAAAACAAACCAATATATGTTTACATTTATGCTTCTCTGTATC 1259
QY 236 -----236
Db 1260 GAATGGTGTTTTAAATACTGATTAATAAAATGTTTGTGCTTAAAAATATAACAATTTATAAT 1319
QY 236 -----236
Db 1320 GTGAGATATTCAAGCATTTCTAATATCAACCGATAAACAACCAAACTGATTTATTAAT 1379
QY 237 -----TrpAspThrProIleHisVal 243
Db 1380 TATTTAACCGGTTTGGTTCGGTTTAAATATATTTGTAGTGGGATACCGCATTCACGTG 1439
QY 244 AspAlaAlaSerGlyGlyPheIleAlaProPheLeuTyrProGluLeuGluTrpAspPhe 263
Db 1440 GACGACGAGCTGGTGGGTTTATTTGCTCCCTTCTTGATCCGACTTGGAGTGGGATTC 1499
QY 264 ArgLeuProLeuValLysSerIleAsnValSerGlyHisLysTyrGlyLeuValTyrAla 283
Db 1500 CGGTACCGTTGGTTAAAGACATAAATGTGAGTGGTCACAAATACGGTTTGGTTTACGCC 1559
QY 284 GlyIleGlyTyrValIleTrpArgAsnLysGluAspLeuProGluLeuLeuIlePheHis 303
Db 1560 GGATCGGTTGGTGGTATGGAGAACCAAAACCGATTTGCTGTAGTGAATTCATCTTCAT 1619
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QY 320 -----320
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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12	2200	84.1	1479	6	AX654603
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14	2199	84.1	1771	8	AF020424
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16	2135.5	81.7	1482	6	AX412801
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Arazi, T., Baum, G., Snedden, W.A., Shelp, B.J. and Fromm, H.				
Molecular and biochemical analysis of calmodulin interactions with				
the calmodulin-binding domain of plant glutamate decarboxylase				
Plant Physiol. 108 (2), 551-561 (1995)				
95334488				
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SULT 2
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SEQUENCE 1810 from Patent WO0216655.
ACCESSION AX507115
VERSION AX507115.1 GI:23389352
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi
1
Harper,J.F., Krebs,J., Wang,X. and Zhu,T.
Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
Patent: WO 0216655-A 1810 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)

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BASE COUNT 432 a 322 c 385 g 370 t

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RIGIN

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Conservative: 0
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Local Similarity: 99.80% Indels: 0
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Gaps: 6

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ACCESSION AX651552
VERSION AX651552.1 GI:29154370
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ORGANISM Arabidopsis thaliana
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsi
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REFERENCE Chang, H.S., Chen, W., Cooper, B., Glazebrook, J., Goff, S.A., Hou, Y.M.,
AUTHORS Katagiri, F., Quan, S., Tao, Y., Whitham, S., Xie, Z., Zhu, T. and Zou, G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 03000898-A 360 03-JAN-2003,
SYNOPSIS Syngenta Participations AG (CH)
FEATURES
source 1. .1509
location/Qualifiers
BASE COUNT 432 a 322 c 385 g 370 t
REGION

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core: 2607.00 Matches: 501
percent Similarity: 99.80% Conservative: 0
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rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
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Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M.,
Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A.,
Tang, C.C., Toriumi, M., Wallender, E.K., Wong, C., Wu, H.C., Yamada, K.,
Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.
Arabidopsis ORF clones
Unpublished
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Cheuk, R., Chen, H., Kim, C.J., Shinn, P., Bowser, L., Carninci, P.,
Chan, M.M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,
Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J.,
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Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
Ecker, J.R.
Direct Submission
Submitted (18-OCT-2002) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN
Arabidopsis Full-length cDNA') : Seki, M., Narusaka, M., Ishida, J.,
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,
Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, PGECC (SSP) Consortium members constructed and
sequenced the PUNI (ORF) clones using the RAFL cDNAs: Cheuk, R.,
Chen, H., Kim, C.J., Shinn, P., Banh, J., Bowser, L., Chan, M.M.,
Chang, B., Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G.,
Lam, B., Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S.,
Palm, C.J., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M.,
Wu, H.C., Yamada, K., Yamamura, Y., Yu, G., Davis, R.W., Theologis, A.,
and Ecker, J.R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to
this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)
contributed equally to this work as PIs.
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 1 (bases 1 to 1813)
 AUTHORS
 Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
 Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
 Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,
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 Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
 Theologis, A. and Ecker, J.R.
 Arabidopsis cDNA clones
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 2 (bases 1 to 1813)
 AUTHORS
 Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J.,
 Bowser, L., Carninci, P., Chang, E., Dale, J.M., Goldsmith, A.D.,
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 Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R.W.,
 Theologis, A. and Ecker, J.R.
 Direct Submission
 Submitted (08-APR-2002) Salk Institute Genomic Analysis Laboratory
 (SIGNAL), Plant Biology Laboratory, The Salk Institute for
 Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
 USA
 RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN
 Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,
 Hayashizaki, Y. and Shinozaki, K.
 The Salk, Stanford, PGECC (SSP) Consortium members carried out the
 sequencing and annotation of the RAFL cDNAs: Shinn, P., Chen, H.,
 Cheuk, R., Kim, C.J., Meyers, M.C., Banh, J., Bowser, L., Chang, E.,
 Dale, J.M., Goldsmith, A.D., Jones, T., Karlin-Neumann, G., Lam, B.,
 Lee, J.M., Lin, J., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
 Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
 Yamada, K., Yamamura, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A.,
 and Ecker, J.R.
 Shinn, P. (SSP/salk) and Seki, M. (RIKEN GSC) contributed equally to
 this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/salk)
 contributed equally to this work as PIs.
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RESULT 6
PETGADY 1785 bp mRNA linear PLN 15-OCT-1993
LOCUS Petunia hybrida glutamate decarboxylase (gad) mRNA, complete cds.
DEFINITION L16797
ACCESSION L16797.1 GI:294111
VERSION glutamate decarboxylase.
KEYWORDS Petunia x hybrida
SOURCE Petunia x hybrida
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Asteridae; Lamids; Solanales; Solanales; Petunia.
1 (bases 1 to 1785)
Baum, G., Chen, Y., Arazi, T., Takatsuki, H. and Fromm, H.
A plant glutamate decarboxylase containing a calmodulin binding
domain. Cloning, sequence, and functional analysis
J. Biol. Chem. 268 (26), 19610-19617 (1993)
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Original source text: Petunia hybrida flower corolla cDNA to mRNA.
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core:          2250.00      Matches:      427
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3-10-006-852-2 (1-502) x PETGAD (1-1785)

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DEFINITION L16977
ACCESSION L16977
VERSION L16977.1 GI:309679
KEYWORDS calmodulin binding protein; glutamate decarboxylase.
SOURCE Petunia x hybrida
ORGANISM Petunia x hybrida
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Petunia.
1 (bases 1 to 1785)
REFERENCE Baum, G., Chen, Y., Arai, T., Takatsuki, H. and Fromm, H.
AUTHORS A plant glutamate decarboxylase containing a calmodulin-binding
TITLE domain: cloning sequence and functional analysis
JOURNAL J. Biol. Chem. (1993) In press

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COMMENT Original source text: Petunia hybrida flower corolla cDNA to mRNA.
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 red. No.: 3.5e-181 Length: 1785
 core: 2250.00 Matches: 427
 percent Similarity: 92.64% Conservative: 39
 est Local Similarity: 84.89% Mismatches: 33
 very Match: 86.04% Indels: 4
 B: 8 Gaps: 2

S-10-006-852-2 (1-502) x PETGLUDECA (1-1785)

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 LOCUS

DEFINITION Nicotiana tabacum glutamate decarboxylase isozyme 1 (NtGAD1) mRNA,
 complete cds.
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 ERSION AF020425.1 GI:3252855
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 REFERENCE 1 (bases 1 to 1705)
 AUTHORS Yun, S.J. and Oh, S.H.
 TITLE Cloning and characterization of a tobacco cDNA encoding
 calcium/calmodulin-dependent glutamate decarboxylase
 JOURNAL Unpublished
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 AUTHORS Yun, S.J.
 TITLE Direct Submission
 JOURNAL Submitted (21-AUG-1997) Faculty of Biological Resources Science,
 Chonbuk National University, 664-14 1-ga Tokjin-dong, Chonju,
 Chonbuk 561-756, South Korea
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RESULT 9
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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Nicotiana tabacum
Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1745)
McLean, M.D., Yevtushenko, D., Deschene, A., Van Cauwenberghe, O.R.,
Makhmoudova, A., Potter, J.W., Bown, A.W. and Shelp, B.J.
Overexpression of glutamate decarboxylase in transgenic tobacco
confers resistance to the northern root-knot nematode
Mol. Breed. 11, 277-285 (2003)
2 (bases 1 to 1745)
McLean, M.D., Yevtushenko, D. and Shelp, B.J.
Direct Submission
TITLE
Submitted (25-APR-2002) Plant Agriculture, University of Guelph,
Guelph, ON N1G 2W1, Canada
FEATURES
Location/Qualifiers
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3-10-006-852-2 (1-502) x AF506366 (1-1745)

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JCUS
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US4774
XRSION
US4774
XWORDS
US4774
XURCE
US4774.1 GI:1777920
XORGANISM
Nicotiana tabacum (common tobacco)
XREFERENCE
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Nicotiana.
1. (bases 1 to 1929)
Dharmasiri,M.A.N., Lu,Y.T. and Harrington,H.M.
Cloning and sequencing of a tobacco cDNA encoding glutamate
decarboxylase
Unpublished
2. (bases 1 to 1929)
Dharmasiri,M.A.N., Lu,Y.T. and Harrington,H.M.
Direct Submission
Submitted (11-APR-1996) M.A. Nihal Dharmasiri, Plant Molecular
Physiology, University of Hawaii, 3190 Maile Way, Honolulu, HI
96822, USA
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Alignment Scores:
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FINITION AF352732 1672 bp mRNA linear PLN 02-MAY-2003
Nicotiana tabacum glutamate decarboxylase isozyme 1 mRNA, complete
cds.
CESSION AF352732
RSION AF352732.1 GI:13310812
YWORDS .
NURCE Nicotiana tabacum (common tobacco)
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiales; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 1672)
Yevrushenko,D., McLean,M.D., Peiris,S.E., Van Cauwenberghre,O.R. and
Shelp,B.J.
Two isoforms of tobacco glutamate decarboxylase are regulated by
calcium/calmodulin and differ in organ distribution
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1672)
AUTHORS Yevrushenko,D., McLean,M.D. and Shelp,B.J.
TITLE Direct Submission

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JOURNAL Submitted (23-FEB-2001) Department of Plant Agriculture, University
of Guelph, Division of Biotechnology, Guelph, Ontario N1G 2W1,
Canada
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Alignment Scores:
Pred. No.: 2,366-179 Length: 1672
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Percent Similarity: 91.65% Conservative: 35
Best Local Similarity: 84.69% Mismatches: 34
Query Match: 85.20% Indels: 8
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US-10-006-852-2 (1-502) x AF352732 (1-1672)
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Submitted (23-FEB-2001) Department of Plant Agriculture, University of Guelph, Division of Biotechnology, Guelph, Ontario N1G 2W1, Canada

Location/Qualifiers

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BASE COUNT 511 a 280 c 392 g 483 t 6 others

ORIGIN

Alignment Scores:

Pred. No.: 2,366-179 Length: 1672

Score: 2228.00 Matches: 426

Percent Similarity: 91.65% Conservative: 35

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Query Match: 85.20% Indels: 8

DB: 8

US-10-006-852-2 (1-502) x AF352732 (1-1672)

QY 1 MetValLeuSerHisAlaValSerGluSerAspValSerValHisSerThrPheAlaSer 20

Db 4 AUGTTCTGTCCAGACACAGCGTCGGAAAGTGAGCTTCCATCCACTTCGATTTCGTTCC 63

QY 21 ArgTyrValArgThrSerLeuProArgPheLysMetProGluAsnSerIleProLysGlu 40

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LOCUS AX654603 1479 bp DNA linear PAT 22-MAR-2003
DEFINITION Sequence 4473 from Patent WO03000898.
ACCESSION AX654603
VERSION AX654603.1 GI:29157417
KEYWORDS Oryza sativa
SOURCE Oryza sativa
ORGANISM Oryza sativa
REFERENCE 1
AUTHORS Chang,H.S., Chen,W., Cooper,B., Glazebrook,J., Goff,S.A., Hou,Y.M.,
Kato,Girir,F., Quan,S., Tao,Y., Whitman,S., Xie,Z., Zhu,T. and Zou,G.
TITLE Plant genes involved in defense against pathogens
JOURNAL Patent: WO 0300898-A 4473 03-JAN-2003;
Syngenta Participations AG (CH)
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Percent Similarity: 90.64%
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VERSION
AY187941.1 GI:28911952
KEYWORDS

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Oryza sativa (japonica cultivar-group)  
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Ehrhartoideae; Oryzaceae; Oryza.  
REFERENCE  
1 (bases 1 to 1502)  
AUTHORS  
Liu, L.L., Zhai, H.Q. and Wan, J.M.  
TITLE  
New rice GAD gene GAD3  
JOURNAL  
Unpublished  
REFERENCE  
2 (bases 1 to 1502)  
AUTHORS  
Liu, L.L., Zhai, H.Q. and Wan, J.M.  
TITLE  
Direct Submission  
JOURNAL  
Submitted (27-NOV-2002) State Key Laboratory of Crop Genetics  
Genome Enhancement, Jiangsu Plant Gene Engineering Research  
Center, Weifang, Nanjing, Jiangsu 210095, P. R. China  
LOCATION/Qualifiers  
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Score: 2200.00 Matches: 420  
Percent Similarity: 90.64% Conservative: 35  
Best Local Similarity: 83.67% Mismatches: 37  
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US-10-006-852-2 (1-502) x AY187941 (1-1502)  
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QY 501 IleCys 502
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AF020424 1771 bp mRNA linear PIN 24-JUN-1998
LOCUS Nicotiana tabacum glutamate decarboxylase isozyme 2 (NtGAD2) mRNA,
DEFINITION complete cds.
ACCESSION AF020424
VERSION AF020424.1 GI:3252853
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 1771)
AUTHORS Yun,S.J. and Oh,S.H.
TITLE Cloning and characterization of a tobacco cDNA encoding
JOURNAL calcium/calmodulin-dependent glutamate decarboxylase
MEDLINE Mol. Cells 8 (2), 125-129 (1998)
PUBMED 9638642
REFERENCE 2 (bases 1 to 1771)
AUTHORS Yun,S.J.
TITLE Direct Submission
JOURNAL Submitted (21-AUG-1997) Faculty of Biological Resources Science,
Chonbuk National University, 664-14 1-ga Tokjin-dong, Chonju,
Chonbuk 561-756, South Korea
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BASE COUNT 548 a 295 c 393 g 535 t
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Alignment Scores:
Pred. No.: 7,24e-177 Length: 1771
Score: 2199.00 Matches: 423
Percent Similarity: 90.8% Conservative: 34
Best Local Similarity: 84.10% Mismatches: 38
Query Match: 84.09% Indels: 8
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US-10-006-852-2 (1-502) x AF020424 (1-1771)
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LOCUS Nicotiana tabacum glutamate decarboxylase isozyme 3 mRNA, complete cds.
DEFINITION
ACCESSION AF353615 GI:13752461
VERSION AF353615.1
KEYWORDS Nicotiana tabacum (common tobacco)
SOURCE Nicotiana tabacum
ORGANISM Nicotiana tabacum
REFERENCE 1 (bases 1 to 1776)
AUTHORS Yevtushenko, D., McLean, M.D., Peiris, S.E., Van Cauwenbergh, O.R. and Shelp, B.J.
TITLE Two isoforms of tobacco glutamate decarboxylase are regulated by calcium/calmodulin and differ in organ distribution
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1776)
AUTHORS McLean, M.D., Yevtushenko, D. and Shelp, B.J.
TITLE Direct Submission
JOURNAL Submitted (26-FEB-2001) Department of Plant Agriculture, University of Guelph, Division of Biotechnology, Bovey Building, Guelph, Ontario N1G 2W1, Canada
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61 AlaSerPheValThrTrpMetGluProGluCysAspLysLeuIleMetSerSerIle 80
269 GCTTCATTTTGACAAACATGATGGACGACGAGTGTGATAGCTTTATGATGGACTCCATT 328
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389 GTGAACATGATAGCAGCTTTATTCAACGCGCCACTAGAAAGAAAGAGACAGCAGTTGGA 448
121 ValGlyThrValGlySerSerGluAlaIleMetLeuAlaGlyLeuAlaPheLysArgLys 140
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Job time : 4597 secs

GenCore version 5.1.6
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1 protein - protein search, using sw model

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(without alignments)
189.764 Million cell updates/sec

tle: US-10-006-852-2

rfect score: 2615

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arched: 629382 seqs, 167460630 residues

tal number of hits satisfying chosen parameters: 629382

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st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2250	86.0	500	15	US-10-006-852-16	Sequence 16, Appl
3	2240	85.7	496	15	US-10-006-852-12	Sequence 12, Appl
4	2226	85.1	496	15	US-10-005-602-2	Sequence 2, Appli
5	2199	84.1	496	15	US-10-006-852-14	Sequence 14, Appl
6	2135.5	81.7	493	15	US-10-006-852-8	Sequence 8, Appli
7	2130	81.5	494	15	US-10-006-852-4	Sequence 4, Appli
8	2080	79.5	500	15	US-10-006-852-6	Sequence 6, Appli
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Sequence 2, Appli
Sequence 11741, A
Sequence 5882, Ap
Sequence 13079, A

ALIGNMENTS

RESULT 1
US-10-006-852-2
; Sequence 2, Application US/10006852
; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kinnersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-006-852-2

Query Match	100.0%;	Score 2615;	DB 15;	Length 502;
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SEQUENCE 16, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kimmersely, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
PRIOR FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 500
TYPE: PRT
ORGANISM: Petunia x hybrida
-10-006-852-16

Query Match 86.0%; Score 2250; DB 15; Length 500;
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1 MVLSHAVSESDSVHSTFASRYVTSLSLPRFKMPNSIPKEAAAYQIINDELMLDGNPRLNL 60
1 MVLKTVSQSDVSIHSTFASRYVTSLSLPRFKMPNSIPKEAAAYQIINDELMLDGNPRLNL 60
61 ASFTVTWMEPECDKLMSSINKNYVDMDEYPTTELQNRQCNVMIHAFNAPLEAEATVG 120
61 ASFTVTWMEPECDKLMSSINKNYVDMDEYPTTELQNRQCNVMIHAFNAPLEAEATVG 120
121 VGTGSSSAIMLAGLAFKRWKQKKAEGKPVDPKNIIVTGANVQVCWEKFAFYFEVELKE 180
121 VGTGSSSAIMLAGLAFKRWKQKKAEGKPVDPKNIIVTGANVQVCWEKFAFYFEVELKE 180
181 VKLSEGYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLNDLLVEKNKETGMDTP 240
181 VKLSEGYVMDPEKAVEMVDENTICVAAILGSTLNGEFEDVKRLNDLLVEKNKETGMDTP 240
241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIGWVWNRKEDLPEEL 300
241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIGWVWNRKEDLPEEL 300
301 IFHINYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
301 IFHINYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGWIVPAYTMPNNAOHIIVLRVV 420
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGWIVPAYTMPNNAOHIIVLRVV 420
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVHKSISLGOEKSESNDNLMTVVKSDIDK 480
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVHKSISLGOEKSESNDNLMTVVKSDIDK 480
481 QRDIIITGWKKFVADRKKTSGIC 502
481 QRDIIITGWKKFVADRKKTSGIC 502

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361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGWIVPAYTMPNNAOHIIVLRVV 420
361 TGRFNIIISKEIGVPLVAFSLKDNROHNEFEISLTLRRFGWIVPAYTMPNNAOHIIVLRVV 420
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVHKSISLGOEKSESNDNLMTVVKSDIDK 480
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVHKSISLGOEKSESNDNLMTVVKSDIDK 480
481 QRDIIITGWKKFVADRKKTSGIC 502
478 QLEMITAWKKFVEEKKKINRVC 500

RESULT 3
US-10-006-852-12
Sequence 12, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kimmersely, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 496
TYPE: PRT
ORGANISM: Nicotiana tabacum
US-10-006-852-12

Query Match 85.7%; Score 2240; DB 15; Length 496;
Best Local Similarity 85.1%; Pred. No. 2.1e-208;
Matches 428; Conservative 35; Mismatches 32; Indels 8; Gaps 3;

1 MVLSHAVSESDSVHSTFASRYVTSLSLPRFKMPNSIPKEAAAYQIINDELMLDGNPRLNL 60
1 MVLKTVASESDSVSIHSTFASRYVTSLSLPRFKMPNSIPKEAAAYQIINDELMLDGNPRLNL 60
61 ASFTVTWMEPECDKLMSSINKNYVDMDEYPTTELQNRQCNVMIHAFNAPLEAEATVG 120
61 ASFTVTWMEPECDKLMSSINKNYVDMDEYPTTELQNRQCNVMIHAFNAPLEAEATVG 120
121 VGTGSSSAIMLAGLAFKRWKQKKAEGKPVDPKNIIVTGANVQVCWEKFAFYFEVELKE 180
121 VGTGSSSAIMLAGLAFKRWKQKKAEGKPVDPKNIIVTGANVQVCWEKFAFYFEVELKE 180
181 VKLSEGYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLNDLLVEKNKETGMDTP 240
181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEFEDVKRLNDLLIEKNKETGMDTP 240
241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIGWVWNRKEDLPEEL 300
241 IHVDAASGGFIAPFLYPELWDFRLPLVKSINVSCHKYGLVYAGIGWVWNRKEDLPEEL 300
301 IFHINYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
301 IFHINYLGADQPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVLREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGWIVPAYTMPNNAOHIIVLRVV 420
361 SGRFNIIISKEIGVPLVAFSLKDSCHTEFEISLTLRRFGWIIIPAYTMPNNAOHIIVLRVV 420
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVHKSISLGOEKSESNDNLMTVVKSDIDK 480
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVHKSISLGOEKSESNDNLMTVVKSDIDK 480
481 QRDIIITGWKKFVADRKKTSGIC 502
474 QLEITTAWKAFVADKKKKNINGVC 496

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; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-006-852-14

Query Match      84.1%; Score 2199; DB 15; Length 496;
Best Local Similarity 84.1%; Pred. No. 2e-204;
Matches 423; Conservative 34; Mismatches 38; Indels 8; Gaps 3;

Qy 1 MVLSHAVSESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRNL 60
Db 1 MVLKSTASESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRNL 60
Qy 61 ASFVTTWMEPECDKLIMSSINKNYVDMDYPTTELQNRVCNMIAHLFNAPLEAEATVG 120
Db 61 ASFVTTWMEPECNTLMDSINKNYVDMDYPTTELQNRVCNMIAHLFNAPLGDGETAVG 120
Qy 121 VGTGSSSEATMLAGLAFKRWQNKRAEGKPVDPKPNIVTGANVOVCWEKFPARYFEVELKE 180
Db 121 VGTGSSSEATMLAGLAFKRWQNKRAEGKPVDPKPNIVTGANVOVCWEKFPARYFEVELKE 180
Qy 181 VKLSEGYVMDPQAVDMDVENTICVADILGSTLNGEFEDVKLNDLLVEKNKETGWDTP 240
Db 181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEFEDVKLNDLLIEKNKETGWDTP 240
Qy 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
Db 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
Qy 301 IFHINYLGADQPTFLNFSKSSQVIAQYQILRLGHEGYRNWMCNENARVLRBIEK 360
Db 301 IFHINYLGADQPTFLNFSKSSQVIAQYQILRLGHEGYRNWMCNENARVLRBIEK 360
Qy 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHTVLRV 420
Db 361 SGFRNIISKEIGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHTVLRV 420
Qy 421 IREDFSRTLAERLVIDIEKVMRELDLPSRVTHKISLGQEKSESNDMLMVTVKSDIDK 480
Db 421 IREDFSRTLAERLVIDIEKVMRELDLPSRVTHKISLGQEKSESNDMLMVTVKSDIDK 480
Qy 481 QRDITIGWKKFVAD-RKKTSGIC 502
Db 474 QLEITTAWLKFAVDKXKKKNGVC 496

RESULT 6
US-10-006-852-8
; Sequence 8, Application US/10006852
; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kimmersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 493
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-006-852-8

; CURRENT FILING DATE: 2002-07-01
; PRIOR APPLICATION NUMBER: US 60/246,367
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 496
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-10-006-852-14

Query Match      85.1%; Score 2226; DB 15; Length 496;
Best Local Similarity 84.7%; Pred. No. 4.9e-207;
Matches 426; Conservative 35; Mismatches 34; Indels 8; Gaps 3;

Qy 1 MVLSHAVSESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRNL 60
Db 1 MVLKSTASESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRNL 60
Qy 61 ASFVTTWMEPECDKLIMSSINKNYVDMDYPTTELQNRVCNMIAHLFNAPLEAEATVG 120
Db 61 ASFVTTWMEPECNTLMDSINKNYVDMDYPTTELQNRVCNMIAHLFNAPLGDGETAVG 120
Qy 121 VGTGSSSEATMLAGLAFKRWQNKRAEGKPVDPKPNIVTGANVOVCWEKFPARYFEVELKE 180
Db 121 VGTGSSSEATMLAGLAFKRWQNKRAEGKPVDPKPNIVTGANVOVCWEKFPARYFEVELKE 180
Qy 181 VKLSEGYVMDPQAVDMDVENTICVADILGSTLNGEFEDVKLNDLLVEKNKETGWDTP 240
Db 181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEFEDVKLNDLLIEKNKETGWDTP 240
Qy 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
Db 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
Qy 301 IFHINYLGADQPTFLNFSKSSQVIAQYQILRLGHEGYRNWMCNENARVLRBIEK 360
Db 301 IFHINYLGADQPTFLNFSKSSQVIAQYQILRLGHEGYRNWMCNENARVLRBIEK 360
Qy 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHTVLRV 420
Db 361 SGFRNIISKEIGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHTVLRV 420
Qy 421 IREDFSRTLAERLVIDIEKVMRELDLPSRVTHKISLGQEKSESNDMLMVTVKSDIDK 480
Db 421 IREDFSRTLAERLVIDIEKVMRELDLPSRVTHKISLGQEKSESNDMLMVTVKSDIDK 480
Qy 481 QRDITIGWKKFVAD-RKKTSGIC 502
Db 474 QLEITTAWLKFAVDKXKKKNGVC 496

RESULT 5
US-10-006-852-14
; Sequence 14, Application US/10006852
; Publication No. US20030046732A1
; GENERAL INFORMATION:
; APPLICANT: Kimmersely, Alan M.
; APPLICANT: Turano, Frank J.
; TITLE OF INVENTION: Methods for Regulating Plant GABA Production
; FILE REFERENCE: 7224-65
; CURRENT APPLICATION NUMBER: US/10/006,852
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Query Match 81.7%; Score 2135.5; DB 15; Length 493;
Best Local Similarity 82.4%; Pred. No. 2.9e-198;
Matches 411; Conservative 32; Mismatches 45; Indels 11; Gaps 2;
1 MVLSHAVSESDVSHSTFASRYVTSLSRPFKMPENSIPKEAAVQIINDELMLDGNPRNL 60
1 MVLKTSVSESDVSHSTFASRYVNSLPRFEMPENSIPKEAAVQIINDELMLDGNPRNL 60
61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTTELQNCRCVNMIAHLFNAPLEBAETA 120
61 ASFTVTWMEPCDKLIMBSINKNYVDMDEYPTTTELQNCRCVNMIAHLFNAPLEBAETA 120
121 VGTGSSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIVTGANVQVCWEKFARYFEVELKE 180
121 VGTGSSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIVTGANVQVCWEKFARYFEVELKE 180
181 VKLSEGYVYMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
181 VNLREDYVYMDPVKAVEMVDENTICVAAILGSTLTGFEFVKLLNDLLVEKNKKTGWDTP 240
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
301 IFHNYLGADQPTTFLNFSKSSQVIAQYQYQIRLGHGEGYRNVMNCRENMIVLREGLEK 360
301 IFHNYLGADQPTTFLNFSKSSQVIAQYQYQIRLGHGEGYRNVMNCRENMIVLREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIPAYTMPNAQHTVLRVV 420
361 TGRFKIVSKENGVPVAFSLKDSCHTEFEISDMRLRYGVIPAYTMPNAQHTVLRVV 420
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVVHKISLQGEKSESNDNLMVTVKSDIDK 480
421 IREDFSRTLAERLVIDIEKVMRELDLPSRVVHKISLQGEKSESNDNLMVTVKSDIDK 480
481 ORDITGWKKFVADRKTTS 499
471 QREVAYWKKUL-ETKTN 488

SULT 7
-10-006-852-4
Sequence 4, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kinnarsely, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 494
TYPE: PRT
ORGANISM: Arabidopsis thaliana
3-10-006-852-4

Query Match 81.5%; Score 2130; DB 15; Length 494;
Best Local Similarity 80.2%; Pred. No. 1e-197;
Matches 404; Conservative 46; Mismatches 42; Indels 12; Gaps 3;
1 MVLSHAVSESDVSHSTFASRYVTSLSRPFKMPENSIPKEAAVQIINDELMLDGNPRNL 60
1 MVLKTSVSESDVSHSTFASRYVNSLPRFEMPENSIPKEAAVQIINDELMLDGNPRNL 59
61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTTELQNCRCVNMIAHLFNAPLEBAETA 120
60 ASFTVTWMEPCDKLIMBSINKNYVDMDEYPTTTELQNCRCVNMIAHLFNAPLEBAETA 119

QY 121 VGTGSSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIVTGANVQVCWEKFARYFEVELKE 180
Db 120 VGTGSSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIVTGANVQVCWEKFARYFEVELKE 179
QY 181 VKLSEGYVYMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
Db 180 VNLSEGYVYMDPQQAQVDMVDENTICVAAILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 239
QY 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300
Db 240 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 299
QY 301 IFHNYLGADQPTTFLNFSKSSQVIAQYQYQIRLGHGEGYRNVMNCRENMIVLREGLEK 360
Db 300 IFHNYLGADQPTTFLNFSKSSQVIAQYQYQIRLGHGEGYRNVMNCRENMIVLREGLEK 359
QY 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIPAYTMPNAQHTVLRVV 420
Db 360 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIPAYTMPNAQHTVLRVV 419
QY 421 IREDFSRTLAERLVIDIEKVMRELDLPSRVVHKISLQGEKSESNDNLMVTVKSDIDK 480
Db 420 IREDFSRTLAERLVIDIEKVMRELDLPSRVVHKISLQGEKSESNDNLMVTVKSDIDK 479
QY 481 Q--RDIITGWKKFVADRKTTS 502
Db 471 EILMEVIVGWRKRFVKKRKGNGVC 494

RESULT 8
US-10-006-852-6
Sequence 6, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kinnarsely, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 500
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-006-852-6

Query Match 79.5%; Score 2080; DB 15; Length 500;
Best Local Similarity 78.8%; Pred. No. 7.3e-193;
Matches 395; Conservative 44; Mismatches 52; Indels 10; Gaps 1;
QY 1 MVLSHAVSESDVSHSTFASRYVTSLSRPFKMPENSIPKEAAVQIINDELMLDGNPRNL 60
Db 1 MVLKTSVSESDVSHSTFASRYVNSLPRFEMPENSIPKEAAVQIINDELMLDGNPRNL 60
QY 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTTELQNCRCVNMIAHLFNAPLEBAETA 120
Db 61 ASFTVTWMEPCDKLIMBSINKNYVDMDEYPTTTELQNCRCVNMIAHLFNAPLEBAETA 120
QY 121 VGTGSSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIVTGANVQVCWEKFARYFEVELKE 180
Db 121 VGTGSSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIVTGANVQVCWEKFARYFEVELKE 180
QY 181 VKLSEGYVYMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
Db 181 VKLSEGYVYMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
QY 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWRNKEDLPEEL 300

241 IHVDAASGGFIAPFLYPLDLEWDFRLPLVKINVSCHKYGLVYAGIGVWVWRTKTDLPDEL 300
301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVIREGLEK 360
301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVIREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDLMLRYGIVPAYTPPNAQHIITVLRVV 420
361 TGRFNIVSKDEGVPLVAFSLKDSCHTEFEISDLMLRYGIVPAYTPPNAQHIITVLRVV 420
421 IREDFSRTLAERLVIDIEKVMRELDELPSRVHKKISLGQKSESNSDNLMTVVKSDIDK 480
421 IREDFSRTLAERLVIDIEKVMRELDELPSRVHKKISLGQKSESNSDNLMTVVKSDIDK 480
481 QRDITIGMKFFVADRKTSGI 501
471 QREVTAYWKKFVDKTDKNGV 491

SEQUENCE 2, Application US/10167547C
Publication No. US20030170653A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
TITLE OF INVENTION: Butyrolactone and its Intermediates
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10167,547C
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/297198
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 2
LENGTH: 498
TYPE: PRT
ORGANISM: Alstroemeria
US-10-006-852-2

Query Match 79.3%; Score 2073; DB 12; Length 498;
Best Local Similarity 77.4%; Pred. No. 3.5e-192;
Matches 391; Conservative 53; Mismatches 51; Indels 10; Gaps 2;

1 MVLGHAVSESDVSVHSTFASRYVRTSLPRFKWPKPENSIPKAEAYQIINDELMDGNPRLN 60
1 MVLSSAVSDNTGPHCTFASRYVRDAPARFMPKENSIPKDTAYQIVNDELMDGNPRLN 60
61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNRQVNMIAHLFNAPLEAEATVG 120
61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNRQVNMIAHLFNAPLEAEATVG 120
121 VGTGSSSAIMLAGLAFKRWQNKRAEGKVPDKNIVTGANVQVCWEKFPARYEVELKE 180
121 VGTGSSSAIMLAGLAFKRWQNKRAEGKVPDKNIVTGANVQVCWEKFPARYEVELKE 180
181 VKLSEGYVMDPQQAQVMDVENTICVADILGSTLNGEFEDVKLLNDLLEKKNKGTGMDT 240
181 VKLSEGYVMDPQQAQVMDVENTICVADILGSTLNGEFEDVKLLNDLLEKKNKGTGMDT 240
241 IHVDAASGGFIAPFLYPLDLEWDFRLPLVKINVSCHKYGLVYAGIGVWVWRTKTDLPDEL 300
241 IHVDAASGGFIAPFLYPLDLEWDFRLPLVKINVSCHKYGLVYAGIGVWVWRTKTDLPDEL 300
301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVIREGLEK 360
301 IFHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVIREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDLMLRYGIVPAYTPPNAQHIITVLRVV 420
361 TGRFNIVSKDEGVPLVAFSLKDSCHTEFEISDLMLRYGIVPAYTPPNAQHIITVLRVV 420

QY 421 IREDFSRTLAERLVIDIEKVMRELDELPSR---VHKISLGQKSESNSDNLMTVVKSD 477
DB 421 IREDFSRTLAERLVIDIEKVMRELDELPSRITTAHVTA-----ENDNGEAVIKKSF 473
QY 478 IDKORDIITGKKFFVADRKTSGIC 502
DB 474 LEIEKKVITHWQDVVWNGKTKNKVC 498

RESULT 10
US-10-006-852-18
Sequence 18, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kimmersely, Alan M.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 502
TYPE: PRT
ORGANISM: Lycopersicon esculentum
US-10-006-852-18

Query Match 77.0%; Score 2014; DB 15; Length 502;
Best Local Similarity 76.0%; Pred. No. 1.9e-186;
Matches 387; Conservative 53; Mismatches 55; Indels 14; Gaps 5;

QY 1 MVL-SHAVSESDVSVHSTFASRYVRTSLPRFKWPKPENSIPKAEAYQIINDELMDGNPRLN 59
DB 1 MVLTTISIRDSSESLHCTFASRYVQEPLEPKFKWPKKMPKAEAYQIVNDELMDGNPRLN 60
60 LASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNRQVNMIAHLFNAPLEAEATVG 119
61 LASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNRQVNMIAHLFNAPLEAEATVG 120
120 GVTGSSSAIMLAGLAFKRWQNKRAEGKVPDKNIVTGANVQVCWEKFPARYEVELK 179
121 GVTGSSSAIMLAGLAFKRWQNKRAEGKVPDKNIVTGANVQVCWEKFPARYEVELK 180
180 EVKLSEGYVMDPQQAQVMDVENTICVADILGSTLNGEFEDVKLLNDLLEKKNKGTGMDT 239
181 EVKLSEGYVMDPQQAQVMDVENTICVADILGSTLNGEFEDVKLLNDLLEKKNKGTGMDT 240
240 PIHVDAASGGFIAPFLYPLDLEWDFRLPLVKINVSCHKYGLVYAGIGVWVWRTKTDLPDE 299
241 PIHVDAASGGFIAPFLYPLDLEWDFRLPLVKINVSCHKYGLVYAGIGVWVWRTKTDLPDE 300
300 LIHINYLGAQDPTFTLNFSGSSQVIAQYQLIRLGHGEGYRNVMENCRENMIVIREGLE 359
301 LVPHINYLGSQDPTFTLNFSGSKSYQIIAQYQLIRLGHGEGYRNVMENCRENMIVIREGLE 360
360 KTRFRNIVSKDEGVPLVAFSLKDSCHTEFEISDLMLRYGIVPAYTPPNAQHIITVLRVV 419
361 KMGREFIVSKDVGVPVAFSLRDSKSYTVFEVSEHLRRFGWIVPAYTPPDAEHIAVLRVV 420
420 VIREDFSRTLAERLVIDIEKVMRELDELPSRVHKKISLGQKSESNSDNLMTVVKSDIDK 473
421 VIREDFSRTLAERLVIDIEKVMRELDELPSRVHKKISLGQKSESNSDNLMTVVKSDIDK 480
474 KKSDDIKQDRIITGKKFFVADRKTSGIC 502
481 -----ETQKDIKHWKRIAG--KKTSGVC 502

RESULT 11
US-10-006-852-10

```
Sequence 10, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kinnersely, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.1
SEQ ID NO 10
LENGTH: 494
TYPE: PRT
ORGANISM: Arabidopsis thaliana
-10-006-852-10

Query Match 75.3%; Score 1969; DB 15; Length 494;
Best Local Similarity 75.2%; Pred. No. 4.2e-182;
Matches 373; Conservative 56; Mismatches 61; Indels 6; Gaps 3;

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1 MVLAV-TNSDSEHLHSTFASRYVTSLSLPRFKWPENSIPKAAAYQIINDELMLDGNPRLNL 59
61 ASFTVTWMEPECDKLIMSSINKNYVDMDEYVTTTELQNRQVNMIAHLFNAPLEAEATVG 120
60 ASFTVTWMEPECDKLIMSSINKNYVDMDEYVTTTELQNRQVNMIAHLFNAPLEAEATVG 119
121 VGTVGSSSEAIMLAGLAFKRWKQKRAEGKPYDKPNIVTGANVQVCWEKFAFYFEVELKE 180
120 CGTVGSSSEAIMLAGLAFKRWKQKRAEGKPYDKPNIVTGANVQVCWEKFAFYFEVELKE 179
181 VKLSEGYVMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
180 VKLSEGYVMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 239
241 IHVDAASGFTAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWIRNKEDLPEEL 300
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301 IFHNYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNVMENCRENMIVLREGLEK 360
300 VFHNYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNVMENCRENMIVLREGLEK 359
361 TERFNIVSKDGVPLVAFSLKSSCHTEFEISDMLRRYGVTPAYTPPNAQHITVLRVV 420
360 TGFKNIVSKDGVPLVAFSLKSSCHTEFEISDMLRRYGVTPAYTPPNAQHITVLRVV 419
421 IREDFSRRLAERLVIDIEKVMRELDELPSRVHIKISLQGEKSESNDMLMTVTKKSDID 480
420 IREDFSRGLADRLIHIQVLKEIGLSRHAHLAA-----AAVSGDDEEVKVKTKMSL 475
481 ORDITGWKKFVADRK 496
476 B-DITKYWKRLVEHKK 490

RESULT 12
US-10-167-547C-4
Sequence 4, Application US/10167547C
Publication No. US20030170653A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/297198
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 6
LENGTH: 529
TYPE: PRT
ORGANISM: Alstroemeria
US-10-167-547C-6
Query Match 71.3%; Score 1864; DB 12; Length 529;
Best Local Similarity 73.3%; Pred. No. 7.3e-172;
Matches 351; Conservative 54; Mismatches 70; Indels 4; Gaps 2;

1 MVLHAVSESDSVHSTFASRYVTSLSLPRFKWPENSIPKAAAYQIINDELMLDGNPRLNL 60

Sequence 10, Application US/10006852
Publication No. US20030046732A1
GENERAL INFORMATION:
APPLICANT: Kinnersely, Alan M.
APPLICANT: Turano, Frank J.
TITLE OF INVENTION: Methods for Regulating Plant GABA Production
FILE REFERENCE: 7224-65
CURRENT APPLICATION NUMBER: US/10/006,852
CURRENT FILING DATE: 2002-07-01
PRIOR APPLICATION NUMBER: US 60/246,367
PRIOR FILING DATE: 2000-11-07
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patent in version 3.1
SEQ ID NO 10
LENGTH: 494
TYPE: PRT
ORGANISM: Arabidopsis thaliana
-10-006-852-10

Query Match 71.3%; Score 1864; DB 12; Length 509;
Best Local Similarity 73.3%; Pred. No. 6.9e-172;
Matches 351; Conservative 54; Mismatches 70; Indels 4; Gaps 2;

1 MVLHAVSESDSVHSTFASRYVTSLSLPRFKWPENSIPKAAAYQIINDELMLDGNPRLNL 60
1 MALSSVSDSNQVQCTYASRYVDRAPGFRMPKPSIPKAAAFMTINDELMDGNPRLNL 60
61 ASFTVTWMEPECDKLIMSSINKNYVDMDEYVTTTELQNRQVNMIAHLFNAPLEAEATVG 120
61 ASFTVTWMEPECDKLIMSSINKNYVDMDEYVTTTELQNRQVNMIAHLFNAPLEAEATVG 120
121 VGTVGSSSEAIMLAGLAFKRWKQKRAEGKPYDKPNIVTGANVQVCWEKFAFYFEVELKE 180
121 CATVGSSEAMLAGLAFKRWKQKRAEGKPYDKPNIVTGANVQVCWEKFAFYFEVELKE 180
181 VKLSEGYVMDPQQAQVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
181 VNLRGYYVMDPEKAVEMVDENTICVAAIIGSTLTGEPEDVKLLNDLLVEKNKKTGWDTP 240
241 IHVDAASGFTAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWVWIRNKEDLPEEL 300
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301 IFHNYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNVMENCRENMIVLREGLEK 360
301 IFHNYLGIDQPTFTLNFSGSNQIIGQYVQIIRLGHGEGYNNVMENCRENMIVLREGLEK 360
361 TERFNIVSKDGVPLVAFSLKSSCHTEFEISDMLRRYGVTPAYTPPNAQHITVLRVV 420
361 MGVEFISDKDIGAPLVIALKSSKHSVFKIADTIRFGWTTIPAYTMPKDVHIAVLVV 420
421 IREDFSRRLAERLVIDIEKVMRELDELPSRVHIKISLQGEKSESNDMLMTVTKKSDID 479
421 IREDFSRRLAERLANDMKVVLVDLHPSRT-----TTIAHVKAVENTGNGYV-IKKSIVE 475

RESULT 13
US-10-167-547C-6
Sequence 6, Application US/10167547C
Publication No. US20030170653A1
GENERAL INFORMATION:
APPLICANT: E.I. du Pont de Nemours and Company
APPLICANT: Damude, Howard G.
TITLE OF INVENTION: A Biological Method for the Production of Alpha-Methylene-Gamma
FILE REFERENCE: CL1804 US NA
CURRENT APPLICATION NUMBER: US/10/167,547C
CURRENT FILING DATE: 2003-03-17
PRIOR APPLICATION NUMBER: 60/297198
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Microsoft Office 07
SEQ ID NO 6
LENGTH: 529
TYPE: PRT
ORGANISM: Alstroemeria
US-10-167-547C-6
Query Match 71.3%; Score 1864; DB 12; Length 529;
Best Local Similarity 73.3%; Pred. No. 7.3e-172;
Matches 351; Conservative 54; Mismatches 70; Indels 4; Gaps 2;

1 MVLHAVSESDSVHSTFASRYVTSLSLPRFKWPENSIPKAAAYQIINDELMLDGNPRLNL 60
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 effect score: 2615
 sequence: 1 MWLSHAVSSDVSHSTFAS.....DIITGKKFVADRKKTSGIC 502
 coring table: BLOSUM62
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 searched: 328717 seqs, 42310858 residues

total number of hits satisfying chosen parameters: 328717

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 Listing first 45 summaries

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 6: /cgn2_6/prodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1023	39.1	466	3	US-09-068-195-25
2	325	12.4	589	4	US-08-939-309-8
3	325	12.4	589	4	US-09-849-180-8
4	325	12.4	589	4	US-09-356-643B-2
5	288	11.0	552	4	US-09-356-643B-11
6	264.5	10.1	542	4	US-08-939-309-6
7	264.5	10.1	542	4	US-09-849-180-6
8	264.5	10.1	542	4	US-09-356-643B-4
9	246.5	9.4	568	4	US-08-939-309-2
10	246.5	9.4	568	4	US-09-849-180-2
11	246.5	9.4	568	4	US-09-356-643B-6
12	227	8.7	568	4	US-08-939-309-4
13	227	8.7	568	4	US-09-849-180-4
14	227	8.7	568	4	US-09-356-643B-8
15	224	8.6	568	3	US-09-328-373-2
16	224	8.6	568	4	US-09-740-369-2
17	160.5	6.1	488	4	US-08-939-309-10
18	160.5	6.1	488	4	US-09-849-180-10
19	160.5	6.1	488	4	US-09-356-643B-10
20	133.5	5.1	525	4	US-09-328-352-4492
21	116	4.4	509	3	US-09-377-557-20
22	107.5	4.1	662	3	US-08-779-814-5
23	105	4.0	729	4	US-09-134-001C-4728
24	104.5	4.0	784	4	US-09-004-838-12
25	101.5	3.9	1221	4	US-09-107-532A-3959
26	101	3.9	730	3	US-09-398-865A-2
27	101	3.9	730	4	US-09-710-714-2

28	100.5	3.8	398	4	US-09-328-352-4507	Sequence 4507, Ap
29	100.5	3.8	544	3	US-08-687-590-30	Sequence 30, Appl
30	99.5	3.8	393	3	US-09-377-557-14	Sequence 14, Appl
31	99.5	3.8	458	4	US-09-134-001C-4422	Sequence 4422, Ap
32	99.5	3.8	529	3	US-09-464-483-2	Sequence 2, Appl
33	99.5	3.8	529	3	US-09-414-664-2	Sequence 2, Appl
34	99	3.8	419	4	US-09-328-352-7844	Sequence 7844, Ap
35	98.5	3.8	1447	4	US-09-376-330-17	Sequence 17, Appl
36	98	3.7	623	4	US-09-107-532A-4726	Sequence 4726, Ap
37	97.5	3.7	402	3	US-09-464-483-4	Sequence 4, Appl
38	97.5	3.7	402	3	US-09-414-664-4	Sequence 4, Appl
39	97	3.7	428	3	US-09-052-778-12	Sequence 12, Appl
40	97	3.7	428	4	US-09-134-001C-4879	Sequence 4879, Ap
41	97	3.7	990	4	US-09-627-376-7	Sequence 7, Appl
42	97	3.7	1120	4	US-09-147-404-1	Sequence 1, Appl
43	96.5	3.7	597	4	US-09-252-991A-32073	Sequence 32073, A
44	95.5	3.7	391	3	US-09-377-557-18	Sequence 18, Appl
45	95.5	3.7	508	4	US-09-858-664A-18	Sequence 18, Appl

ALIGNMENTS

RESULT 1
 ; Sequence 25, Application US/09068195B
 ; Patent No. 6140078
 ; GENERAL INFORMATION:
 ; APPLICANT: Sanders, Jan W.
 ; APPLICANT: Ledebos, Adrianus M.
 ; APPLICANT: Venema, Gerard
 ; APPLICANT: Kok, Jan
 ; TITLE OF INVENTION: Salt-Inducible Promoter Derivable from a Lactic Acid Bacterium, and Its Use in a Lactic Acid Bacterium for
 ; TITLE OF INVENTION: Production of Desired Protein
 ; FILE REFERENCE: Sanders-60113/0252227
 ; CURRENT APPLICATION NUMBER: US/09/068,195B
 ; CURRENT FILING DATE: 1998-07-29
 ; EARLIER APPLICATION NUMBER: PCT/EP97/04755
 ; EARLIER FILING DATE: 1997-08-20
 ; EARLIER APPLICATION NUMBER: EP 97200744/7
 ; EARLIER FILING DATE: 1997-03-13
 ; EARLIER APPLICATION NUMBER: EP 96202444/4
 ; EARLIER FILING DATE: 1996-09-05
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 25
 ; LENGTH: 466
 ; TYPE: PRT
 ; ORGANISM: L. lactis MGI363
 ; US-09-068-195-25

Query Match	39.1%;	Score 1023;	DB 3;	Length 466;
Best Local Similarity	45.0%;	Pred. No. 8.3e-95;		
Matches	195;	Conservative	Mismatches 142;	Indels 6;
Gaps	3;			
Qy	18	FASRYVTSLPRFKMENSIPKEAAIQIINDELMDCNPRNLASFTVTWMEPCDKLIM	77	
Db	18	FGSESEQVDFPKYLAQOQSTIEPRVAYQLVQDEMDLDEGNARLNLAATFCQTYMEPEAVKLMS	77	
Qy	78	SSINKNVDMDEYPTTTELONRCVNMIAHLFNAPLEAEATVGVGTGVSSEATMLAGLAF	137	
Db	78	QTEKNAIDKSEFPRTEENRCVNMIAOLWNA--SEKGIYGTSTIGSSEACNCGMMAL	135	
Qy	138	KRWQNKRRKAEKFPD--KPNIVTGANVQVCEKFARYFEVELKEVKLSEGYVMDPQA	195	
Db	136	KFSWRKRAEKLGLDINAKPNLVISGYQVCEKFCVYWDIEMREVPMDREHMSINLEKV	195	
Qy	196	VDWVDENTICVADILGSLNGEFEDVKLNDLLVEKNKGTGWDTPHVDAAAGGFAPL	255	
Db	196	MDVYETTCIGVGMINGITTYGRYDDIKALDNLNIEYKQTDYKVIYHVDAAAGGLYAPV	255	
Qy	256	YPELEMDFRPLVKSINVSQHKYGLVAGVIGWYWRNKEDLPBELIFHINYLGAQDPTFT	315	

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||||| 256 EBELEWDFELXNVISINTSGHYGLVPGVGNLWDRKKYLPEELIFKVSJLGGELPTMA 315
||||| 316 LNFSGSSVIAQYQILRLGHEGRNVNENCRNMIVLREGLEKTERFNIVSKDEGVPL 375
||||| 316 INFHSASOLIQYFNVRVYGDGYKAIHERTHKVMYLAEEIEKTGMFEIMNDGAQLPI 375
||||| 376 VAFSLKDSCH--TFEISDMLRRYGVIPAYTPMPPNAQHITVLRVIREDFSRTLAERL 433
||||| 376 VCYKUKENSRWNLYDIADRLMKGWQVPAYPLPNLENLIIQLVIRADFGNMAFNY 435
||||| 434 VIDLEKVMFELDE 446
||||| 436 VQDMQRAIDALNK 448

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RESULT 2

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3-08-939-309-8
Sequence 8, Application US/08939309
Patent No. 6423527
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Maki J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116.402
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-939-309-8

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Query Match 12.4%; Score 325; DB 4; Length 589;
Best Local Similarity 24.7%; Pred. No. 6.2e-24;
Matches 122; Conservative 98; Mismatches 188; Indels 86; Gaps 20;
3 LSHAVSESDVSVHSTFASRYVR--TSLPRF-KNPENSIFKEAYQIINDELMDGNPLRN 59
106 LRGTVEKVKVQKQSDIELRISDSQIANNFPQLPSNGIPQDDVIELN-----KLN 156
60 LASVTTWMEPEC-----DKLWSSIN-----KNYVDWDEYPTVTEQLONRCVNM 104
157 DLTPHTQWKEGKGVSGVYHGGDLHLQIAYEKYCVANQLHPDVPFPAVKMESEVSVW 216
105 AHUFNAPLEAEATVGVTVGSSEAMLAGLAFKRWQNKRAEKVPDKPNIVTGANVQ 164
217 LRMFNAP---SDTCGCGTTTSGGTESULLACLAKMYALHHR-----GITEPEIIAFVTAH 268

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QY 165 VCWEKFARYFEVELKEVKLSEGYVYMDPQAAVDMVDENTICVADILGSTLN---GEFBDV 221
DB 269 AGFDKAAVYFGKLRHVELDPTTYQVDLKGKVKFKINKTIL---LVGSAPFPFGIADDI 325
QY 222 KLNDLLVKNKTKETGMDPTIHVDAASGGGFIAPFL---YPELE-WDFRLPLVKSLNVSGH 276
DB 326 EGLGK-IAQKYK-----LPLHVDSCIGSGFIVSFMEKAGYKNLPLLDFFRVPGVTSICDTH 379
QY 277 KYGLVYAGIGWIRNKEDLPEELIFHINYLGAQDPTTLNFSKSSOVIAQYQYLIIRLG 336
DB 380 KYGFAPKSGSVIMIRNSDLMHQYVYNPAWTGELGSGPTLAGSRECAIVGCVATWANG 439
QY 337 HEGYRNVMENCRNMIVLREGLEKTERFNI-----VSKDEGVPLVAFSLKDSCHTEFEIS 392
DB 440 ENGYY--IESQEB-IVGAAMKFKYIQENIPDLNMGNPRYSVIFSFKTLNIH---ELS 492
QY 393 DMLRRYGVIPAYTPMPPNAQHITVLRVIREDFSRTLAERLVIDIEKVMRELDLPSRVI 452
DB 493 DRLSKKGWHFNALQKP-----VALHVAFTLR-LSAHVVDVEICDILR----- 531
QY 453 HKISLGOEKSESN 466
DB 532 --TTVQELKSESN 543

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RESULT 3

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US-09-849-180-8
Sequence 8, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 589 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-849-180-8

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Query Match 12.4%; Score 325; DB 4; Length 589;
Best Local Similarity 24.7%; Pred. No. 6.2e-24;
Matches 122; Conservative 99; Mismatches 188; Indels 86; Gaps 20;

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352 IYLRGKTERNIVSKDEGVLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNA 411
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 412 QHITVLVRVIRDFSTLAERLVIDIEKVMRELDLPSRVHVKISLGOEKSESND--N 468
 477 IHICLTINQANEVNAFA---VDLEKICEEL-----AAKGQKADSGMAAMYG 522
 469 LMVTVKSDIDK 480
 523 MAAQVPKSVUDE 534

RESULT 6
 3-08-939-309-6
 Sequence 6, Application US/08939309
 Patent No. 6423527
 GENERAL INFORMATION:
 APPLICANT: Saba, Julie D.
 APPLICANT: Zhou, Jianhui
 TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 TITLE OF INVENTION: METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED AND BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/939,309
 FILING DATE: 29-SEP-1997
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: David, Maki J.
 REGISTRATION NUMBER: 31,392
 REFERENCE/DOCKET NUMBER: 200116.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 542 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 -08-939-309-6

Query Match 10.1%; Score 264.5; DB 4; Length 542;
 Best Local Similarity 22.3%; Pred. No. 7.2e-18;
 Matches 109; Conservative 93; Mismatches 207; Indels 79; Gaps 20;

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 135 VFNREDDKDEREMVEYVFGKFAWNLPLNPKL-----PPGVRIAEAVRMC 180
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 165 VCWKFARYFEVELKVKLSEGYVMDPOQAVMDVENTICVADILGSTLN---GEFEDV 221

Db 231 AAFFKAAECFRIVKRKI PVDVTFKVDLVKMAAINKRT-CM--LVGSAPNFPFGTVDDI 287
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 Db 288 EAIGQLGLE-----YDIPVHVDAICLGGLLPFLFEEDIRYDFRVPGVSSISADSHKYGL 341
 QY 281 VYAGIGWIVRNKEDLPBELIFHINYLGAQDPTFTLNFSGSSQVIAQYQIIRLHGEGY 340
 Db 342 APKSSVVLRYRNKELLHNQYFCDADWQGGIYASATMEGSRAGHNIALCWAAMLYHAQSGY 401
 QY 341 ----RNVMCNRENMIVLREGLEKTERFNIVSKDEGVLVAFSLKDSCHTEFEISDMLR 396
 Db 402 KANARKIVDTTRK---IRNGLSNIKGKLGQSPD-VCIIVSWTNDGV--ELYRPHFMK 454
 QY 397 RVGVIPAYTMPNPAQHITVLVRVIREDFSRILAERLVIDIEKVMRELDLPSRVHVKIS 456
 Db 455 EKHQNLNGLOFPAGV-HI-----MVTNHTHPLGLAEAFVADCAAEVFEVKS-----HKPS 503
 QY 457 LGOEKSES 464
 Db 504 ESDKTSEA 511

RESULT 7
 US-09-849-180-6
 Sequence 6, Application US/09849180
 Patent No. 6495359
 GENERAL INFORMATION:
 APPLICANT: Saba, Julie D.
 APPLICANT: Zhou, Jianhui
 TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed Intellectual Property Law Group
 STREET: 701 Fifth Avenue, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98055

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/849,180
 FILING DATE: 04-May-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Pepe, Jeffrey C.
 REGISTRATION NUMBER: 46,985
 REFERENCE/DOCKET NUMBER: 200116.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 542 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-849-180-6

Query Match 10.1%; Score 264.5; DB 4; Length 542;
 Best Local Similarity 22.3%; Pred. No. 7.2e-18;
 Matches 109; Conservative 93; Mismatches 207; Indels 79; Gaps 20;

3 LSHAVSESDVSVHSTFASRYVRTSLPRFKPENSIPKEAA-YQINDELMLDGNFRLNLA 61
 77 LNEVKDELEKSLRIVDRSTVEYFTIPSHSVGRTEVLRLAAIYDDLGPAFLG--RVSGA 134

RESULT 9

; Patent No. 6423527

APPLICANT: Saba, Julie D.

TITLE OF INVENTION: POLYPEPTIDES

```

; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:

```

STREET: 6300 Columbia Center,

STATE: Washington
COUNTRY: USA

; COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CURRENT APPLICATION DATA:

FILING DATE: 29-SEP-1997

NAME: David, Maki J.

; REFERENCE/DOCKET NUMBER: 2001-
EST DOCKET OR PETIT INTRODUCTION

TELEFAX: (206) 682-6031

SEQUENCE CHARACTERISTICS:

NAME: amino acid
TOPOLOGY: linear

US-08-939-309-2

Query Match	9.4%	Score
Best Local Similarity	23.2%	Precedence

113 WUKT-----I PBOCMCTA EWT FI :
|||:| : :
|||:| : :

Qy 82 K - - - - NYVDMDEYPVTTTELQNRCV

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b      166 EFTWSNPLHPDIIPGLRKLAEIVRMTCSLFGNG-----GPDSCGCVTSGGTESILMACRAY 221
y      138 KRKQWNRKRAEGKPVDPKPNIVTGANVQVCKEFPARYFEVELKEVKLSGGYVYMDPQQAVD 197
b      222 -----RDLALEKGIKTPEIVAPESAHAAFDKAAHYFGMKIVRVALKKMNEV-DYQAMKR 274
y      198 MVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTPIHVDAASGGFIAFFL-- 255
b      275 AISRNTAMLCVSTPQPHGVMDPVEVAKLTVR-----YKPLHVDACLGGFLVFMKEK 328
y      256 --Yp-ELEWDFRLPLVKSINVSGHKYGLVYAGIGWVWNRKEDLPEELIFHINYLGADQP 312
b      329 AGYPLEKPFDFRVKGVTSISADTHKYGAPKSSVVMYSNEKYRTYQFFVGADMQGGVYA 388
y      313 TFLNPSKSSQVIAQYQYQIRLGHGEGYRNVNENMIVLREGLEKTERENIVYSKDEG 372
b      389 SPSTAGSRPGIITACWAAALMHFGENGIVEATKQIIKTARFLKSELENKTNIFIFG-DPQ 447
y      373 VPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNNAQHITVLRVVIREDFSRTLAER 432
b      448 LSVIALGSNDFDI---YRLSNMWSAKGNF-NYLOPPRSIHFCITLVHTR-----KR 495
y      433 LVVIDIEKWMRE 443
b      496 VAIQFLKDIRE 506

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RESULT 10

3-09-849-180-2

Sequence 2, Application US/09849180

Patent No. 6495359

GENERAL INFORMATION:

APPLICANT: Saba, Julie D.

APPLICANT: Zhou, Jianhui

TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seed Intellectual Property Law Group

STREET: 701 Fifth Avenue, Suite 6300

CITY: Seattle

STATE: Washington

COUNTRY: USA

ZIP: 98055

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/849,180

FILING DATE: 04-May-2001

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Pepe, Jeffrey C.

REGISTRATION NUMBER: 46,985

REFERENCE/DOCKET NUMBER: 200116.402

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 622-4900

TELEFAX: (206) 692-6031

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 568 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

-09-849-180-2

Query Match 9.4%; Score 246.5; DB 4; Length 568;

Best Local Similarity 23.2%; Pred. No. 5.2e-16;

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Matches 100; Conservative 76; Mismatches 210; Indels 45; Gaps 12;
Qy 22 YVRTSLPRFKWPENSIPKEAAVQIINDELMNGNPRNLINLASPVTTWMEPCDKLIMSSIN 81
Db 112 YVKT-----LPAQGMGTAEVLERLKEYSSMDGSMQEGKASGAVYNGEPKLTLLVQAYG 165
Qy 82 K---NYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEATAVGVGTGVSSEAIMLAGLAF 137
Db 166 EFTWSNPLHPDIIPGLRKLAEIVRMTCSLFGNG-----GPDSCGCVTSGGTESILMACRAY 221
Qy 138 KRKQWNRKRAEGKPVDPKPNIVTGANVQVCKEFPARYFEVELKEVKLSGGYVYMDPQQAVD 197
Db 222 -----RDLALEKGIKTPEIVAPESAHAAFDKAAHYFGMKIVRVALKKMNEV-DYQAMKR 274
Qy 198 MVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTPIHVDAASGGFIAFFL-- 255
Db 275 AISRNTAMLCVSTPQPHGVMDPVEVAKLTVR-----YKPLHVDACLGGFLVFMKEK 328
Qy 256 --Yp-ELEWDFRLPLVKSINVSGHKYGLVYAGIGWVWNRKEDLPEELIFHINYLGADQP 312
Db 329 AGYPLEKPFDFRVKGVTSISADTHKYGAPKSSVVMYSNEKYRTYQFFVGADMQGGVYA 388
Qy 313 TFLNPSKSSQVIAQYQYQIRLGHGEGYRNVNENMIVLREGLEKTERENIVYSKDEG 372
Db 389 SPSTAGSRPGIITACWAAALMHFGENGIVEATKQIIKTARFLKSELENKTNIFIFG-DPQ 447
Qy 373 VPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNNAQHITVLRVVIREDFSRTLAER 432
Db 448 LSVIALGSNDFDI---YRLSNMWSAKGNF-NYLOPPRSIHFCITLVHTR-----KR 495
Qy 433 LVVIDIEKWMRE 443
Db 496 VAIQFLKDIRE 506

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RESULT 11

US-09-356-643B-6

; Sequence 6, Application US/09356643B

; Patent No. 6569666

; GENERAL INFORMATION:

; APPLICANT: Saba, Julie D.

; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,

; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND

; TITLE OF INVENTION: METHODS OF USE THEREFOR

; FILE REFERENCE: 200116.402C1

; CURRENT APPLICATION NUMBER: US/09/356,643B

; CURRENT FILING DATE: 1999-07-19

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 568

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-356-643B-6

Query Match

9.4%; Score 246.5; DB 4; Length 568;

Best Local Similarity 23.2%; Pred. No. 5.2e-16;

Matches 100; Conservative 76; Mismatches 210; Indels 45; Gaps 12;

Qy 22 YVRTSLPRFKWPENSIPKEAAVQIINDELMNGNPRNLINLASPVTTWMEPCDKLIMSSIN 81

Db 112 YVKT-----LPAQGMGTAEVLERLKEYSSMDGSMQEGKASGAVYNGEPKLTLLVQAYG 165

Qy 82 K---NYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEATAVGVGTGVSSEAIMLAGLAF 137

Db 166 EFTWSNPLHPDIIPGLRKLAEIVRMTCSLFGNG-----GPDSCGCVTSGGTESILMACRAY 221

Qy 138 KRKQWNRKRAEGKPVDPKPNIVTGANVQVCKEFPARYFEVELKEVKLSGGYVYMDPQQAVD 197

Db 222 -----RDLALEKGIKTPEIVAPESAHAAFDKAAHYFGMKIVRVALKKMNEV-DYQAMKR 274

Qy 198 MVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTPIHVDAASGGFIAFFL-- 255

275 ALSRNTAMLVSTPOPPHGVMDPVEVAKLTVR-----YKILPHVDACLGGLFVIMFK 328
256 --YP-ELEWDFRLPLVUKSINVSCHKYGLVYAGIGWVIWRNKEDLPEELIFHINILGADQP 312
329 AGYPLEKEPFRVKGVTISADTHKYGVAPKSSVWVMSNEKYTYQFFVGADQGGVYA 388
313 TFTLNFSGSSQVIAQYQLIRLHGHEGRVNMENCRENMIVLREGLEKTERFNTVSKDEG 372
389 SPISIAGSRFGIIAACMAALMHFGNGYVEATKQIIKTAREFLKSELENIKNIFIFG-DPQ 447
373 VPLVAFSLKDSCHTEFEISDMLRRYGIVPAYTTPPNAQHITVLRVVIDRFSRTLAER 432
448 LSVIALGSDNFDI---YRLSNMWSAKGNF-NYLOFPRSIFHCITLVHTR-----KR 495
433 LVVIDIEKVMRE 443
496 VAIQFLKDIRE 506

RESULT 12
US-08-939-309-4
Sequence 4, Application US/08939309
Patent No. 6423527
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Maki J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200115.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-939-309-4

Query Match 8.7%; Score 227; DB 4; Length 568;
Best Local Similarity 21.6%; Pred. No. 4.9e-14;
Matches 98; Conservative 84; Mismatches 212; Indels 60; Gaps 14;

8 SESDVSVHSTFA---SRVYRTSLPRFKPENSIPKEAAAYQIINDELMLDGNPRLNLASFV 64
95 TKDDISKMSFLKVDKEYKA-----LPSQGLSSSAVLEKLEYSSNDATFQGRASGT 148
65 TTWMEPCDKLIMSSIN-----KQYVMDDEYPVTTELQRCVNMIAHLNAPLEAEATVG 120
149 VYSGBEKLTELIVKAGDGFAMSNPLHPLDIFPLGLRKIEAEIVRIACSLFNG----GPDSCG 204

QY 121 VGTVGSEAIMLA-----GLAFKRKWNKRKAEGKPVDPKPNITVGANVQVCWEKFARFEE 175
DB 205 CVTSGGTESILMACKACRDIAFE-----KGIKTPEIVAPQSAHAFAFNKAASYFG 253
QY 176 VELKEYKLGSEGYVMDPQOAVDMVDENTICVADILGSLTNGFEFDVKLLNDLLVEKNKET 235
DB 254 MKTVRVPFLTMMEV-DVRAMRAISRNTAMLVCSPTFPQFPFHGVDPVPEVAKLAVK----- 307
QY 236 GMDTPHVDAAAGGFIAPFL-----YP-ELEWDFRLPLVUKSINVSCHKYGLVYAGIGWVIW 290
DB 308 -YKILPHVDACLGGLFVIMFKAGYPLEHPDFRVRKGVTSISADTHKYGVAPKSSLVLY 366
QY 291 RNKEDLPEELIFHINILGADQPTFTLNFSGSSQVIAQYQLIRLHGHEGRVNMENCREN 350
DB 367 SDKKYRNYQFFVTDWQGGIYASPTIAGSRPGGISAAWAAALMHFGNGYVEATKQIIKT 426
QY 351 MIVLREGLEKTERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGIVPAYTTPPN 410
DB 427 ARFLKSELENIKGIFVFGNPQ-LSLIALGSRDFDI---YRLSNLMTAKGNLNLQLOFPFS 482
411 AQH-ITVLRVVIDRFSRTLAERLVIDIEKVMRE 443
483 IHFCITLLEA-----RKRVAIQFLKDIRE 506

RESULT 13
US-09-849-180-4
Sequence 4, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-849-180-4

Query Match 8.7%; Score 227; DB 4; Length 568;
Best Local Similarity 21.6%; Pred. No. 4.9e-14;
Matches 98; Conservative 84; Mismatches 212; Indels 60; Gaps 14;

8 SESDVSVHSTFA---SRVYRTSLPRFKPENSIPKEAAAYQIINDELMLDGNPRLNLASFV 64

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b      95 TKDDISKNMFLKVDKEYVKA-----LPSQGLSSSAVLEKKEYSSMDAFWQGRASGT 148
      65 TTWMEPCDKLIMSSIN----KNYVDMDEYPTTELQNCRCVNMIAHLFNAPLEAEATVG 120
      149 VYSGEEKLTLLKAYGDFAWSNPLHPDIFPGLRKTAEIVRIACSLFNG----GPDSCG 204
      121 VGTVGSSEAIMLA-----GLAFKKQWKKKASGKPVDRKNIIVTGANVQVCWEKARYPE 175
      205 CVTSGGTESILMACCRDLAFE-----KGIKTPEIAPQSAHAANFKKASVFG 253
      176 VELKEVKLSEGYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLNDLLVEKNKET 235
      254 MKIVRPLTKMVEV-DVRAMRRAISRNTAMLCVSTPQPHGVIDPVEVAKLAVK----- 307
      236 GWDTPIHVDAASGGFIAPFL-----YP-ELEWDPRPLVKSINVSCHKYGLVYAGIGWIW 290
      308 -YKLPFHVDACLGGLFLIVFWEKAGYPLEHPDFRVKGVTSISADTHKYGYAPKGSLSLVLY 366
      291 RNKEDLPEELIFHINYLADQPTFTLNFSGSSQVIAQYYQLIRLGHGEGYRNVMNCREN 350
      367 SDKRYRNVQFFVDTWQGGIYASPTIAGSRPGGISAAACWAALMHFGENGVEATKQIIKT 426
      351 MIVLREGLEKTERNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMBPN 410
      427 ARFLKSELENIKGIFVFGNPQ-LSLIALGSRDFDI---YRLSNLMTAKGNLNLQLOFPF 482
      411 AQH-ITVLRVIREDFSRTLAERLVIDIEKVMRE 443
      483 IHFCITLLHA-----RKVAIQFLKDIRE 506

RESULT 14
3-09-356-643B-8
Sequence 8, Application US/09356643B
Patent No. 6569666
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402C1
CURRENT APPLICATION NUMBER: US/09/356.643B
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 568
TYPE: PRT
ORGANISM: Homo sapiens
-09-356-643B-8

Query Match      8.7%; Score 227; DB 4; Length 568;
Best Local Similarity 21.6%; Pred. No. 4.9e-14;
Matches 98; Conservative 84; Mismatches 212; Indels 60; Gaps 14;

      8 SEDSVSHSTFA---SRYVTSLSLPRFKMPENSIPKEAAVQIINDELMLDGNRLNLASFV 64
      95 TKDDISKNMFLKVDKEYVKA-----LPSQGLSSSAVLEKKEYSSMDAFWQGRASGT 148
      65 TTWMEPCDKLIMSSIN----KNYVDMDEYPTTELQNCRCVNMIAHLFNAPLEAEATVG 120
      149 VYSGEEKLTLLKAYGDFAWSNPLHPDIFPGLRKTAEIVRIACSLFNG----GPDSCG 204
      121 VGTVGSSEAIMLA-----GLAFKKQWKKKASGKPVDRKNIIVTGANVQVCWEKARYPE 175
      205 CVTSGGTESILMACCRDLAFE-----KGIKTPEIAPQSAHAANFKKASVFG 253
      176 VELKEVKLSEGYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLNDLLVEKNKET 235
      254 MKIVRPLTKMVEV-DVRAMRRAISRNTAMLCVSTPQPHGVIDPVEVAKLAVK----- 307
      236 GWDTPIHVDAASGGFIAPFL-----YP-ELEWDPRPLVKSINVSCHKYGLVYAGIGWIW 290
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Db      308 -YKLPFHVDACLGGLFLIVFWEKAGYPLEHPDFRVKGVTSISADTHKYGYAPKGSLSLVLY 366
      291 RNKEDLPEELIFHINYLADQPTFTLNFSGSSQVIAQYYQLIRLGHGEGYRNVMNCREN 350
      367 SDKRYRNVQFFVDTWQGGIYASPTIAGSRPGGISAAACWAALMHFGENGVEATKQIIKT 426
      351 MIVLREGLEKTERNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMBPN 410
      427 ARFLKSELENIKGIFVFGNPQ-LSLIALGSRDFDI---YRLSNLMTAKGNLNLQLOFPF 482
      411 AQH-ITVLRVIREDFSRTLAERLVIDIEKVMRE 443
      483 IHFCITLLHA-----RKVAIQFLKDIRE 506

RESULT 15
US-09-238-373-2
Sequence 2, Application US/09238373A
Patent No. 6187562
GENERAL INFORMATION:
APPLICANT: DUCKWORTH, DAVID MALCOLM
APPLICANT: GODDEN, ROBERT JAMES
APPLICANT: TESTA, TANIA TAMSON
TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30034
CURRENT APPLICATION NUMBER: US/09/238,373A
CURRENT FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: UK 9824026.0
EARLIER FILING DATE: 1998-11-03
EARLIER APPLICATION NUMBER: EP 98300625.5
EARLIER FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 568
TYPE: PRT
ORGANISM: Homo sapiens
US-09-238-373-2

Query Match      8.6%; Score 224; DB 3; Length 568;
Best Local Similarity 21.4%; Pred. No. 9.9e-14;
Matches 96; Conservative 86; Mismatches 217; Indels 50; Gaps 13;

      8 SEDSVSHSTFA---SRYVTSLSLPRFKMPENSIPKEAAVQIINDELMLDGNRLNLASFV 64
      95 TKDDISKNMFLKVDKEYVKA-----LPSQGLSSSAVLEKKEYSSMDAFWQGRASGT 148
      65 TTWMEPCDKLIMSSIN----KNYVDMDEYPTTELQNCRCVNMIAHLFNAPLEAEATVG 120
      149 VYSGEEKLTLLKAYGDFAWSNPLHPDIFPGLRKTAEIVRIACSLFNG----GPDSCG 204
      121 VGTVGSSEAIMLAGLAFKKQWKKKASGKPVDRKNIIVTGANVQVCWEKARYPEVKE 180
      205 CVTSGGTESILMACKAY-----RDLAFKGIKTPEIAPQSAHAANFKKASVFGKIVR 258
      181 VKLSEGYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLNDLLVEKNKETGWDTP 240
      259 VPLTKMVEV-DVRAMRRAISRNTAMLCVSTPQPHGVIDPVEVAKLAVK-----YKIP 311
      241 IHVDAASGGFIAPFL-----YP-ELEWDPRPLVKSINVSCHKYGLVYAGIGWIWRENKED 295
      312 LHVDACLGGLFLIVFWEKAGYPLEHPDFRVKGVTSISADTHKYGYAPKGSLSLVSDKY 371
      296 LPBELPHINYLADQPTFTLNFSGSSQVIAQYYQLIRLGHGEGYRNVMNCRENIVLR 355
      372 RNYQFFVDTWQGGIYASPTIAGSRPGGISAAACWAALMHFGENGVEATKQIIKTAREFLK 431
      356 EGGLEKTERNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMBPNQAH-I 414
      432 SELENIKGIFVFGNPQ-LSVIALGSRDFDI---YRLSNLMTAKGNLNLQLOFPF 487
      415 TVLRVIREDFSRTLAERLVIDIEKVMRE 443
```

||:| | | | |
488 TILHA-----RKRVAIQFLKDIRE 506

arch completed: October 22, 2003, 15:09:32
b time : 43 secs

encoding a plant glutamic acid decarboxylase enzyme into plant's genome

Claim 17; Page 53; 63pp; English.

The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAD), to provide a transformed plant that expresses the GAD coding sequence in response to a signal. Plants of this type have an enhanced ability to tolerate environmental or other stresses. The present sequence is the A. thaliana GAD1 protein.

Sequence 502 AA;

Query Match 100.0%; Score 2615; DB 23; Length 502;
Best Local Similarity 100.0%; Pred. No. 1.4e-241;
Matches 502; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MVLHSAVSDSVHSTFASRYVTSLSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
1 MVLHSAVSDSVHSTFASRYVTSLSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATAVG 120
61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATAVG 120
121 VGTGVSSEAIMLAGLAFKRWQKKAEGKPVDPKNIVTGANVQVCWEKFPARYFEVELKE 180
121 VGTGVSSEAIMLAGLAFKRWQKKAEGKPVDPKNIVTGANVQVCWEKFPARYFEVELKE 180
181 VKLSEGYVMDPQAAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
181 VKLSEGYVMDPQAAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKINSVGHKYLTVAGIWNKEDLPEEL 300
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKINSVGHKYLTVAGIWNKEDLPEEL 300
301 IFHINYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNWNCNEMIVLREGLEK 360
301 IFHINYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNWNCNEMIVLREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHIITVLRV 420
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHIITVLRV 420
421 IREDFSRTLAERLVIDIEKVMRELDLPSPRVTHKISLGQEKSESNDLMVTVKKSDDIK 480
421 IREDFSRTLAERLVIDIEKVMRELDLPSPRVTHKISLGQEKSESNDLMVTVKKSDDIK 480
481 QRDIIITGWKKFVADRKKTSGIC 502
481 QRDIIITGWKKFVADRKKTSGIC 502

RESULT 2
ABB93521 standard; Protein; 502 AA.

ABB93521;

31-MAY-2002 (first entry)

Herbicide active polypeptide SEQ ID NO 2732.

Herbicide; plant; agriculture; herbicide.

Arabidopsis thaliana.

WO200210210-A2.

XX PD 07-FEB-2002.
XX PF 28-AUG-2001; 2001WO-EP09892.
XX PF 28-AUG-2001; 2001WO-EP09892.
XX PA (FARB) BAYER AG.
XX PI Tietjen K, Weidler M;
XX DR WPI; 2002-269010/31.
XX PT Identifying plant target proteins for herbicidally active compounds,
XX PT comprising aligning and comparing nucleic acid or amino acid sequences
XX PT from plant with nucleic acid or amino acid sequences from non-plant
XX PT organisms -
XX FS Claim 5; SEQ ID NO 2732; 261pp + Sequence Listing; English.
XX CC The invention relates to identifying target proteins
XX CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
XX CC aligning and comparing nucleic acid or amino acid sequences from plant
XX CC with nucleic acid or amino acid sequences from non-plant organisms using
XX CC suitable search parameters, where plant sequences having an E-value
XX CC greater by a factor of 3 than the E-value of most similar non-plant
XX CC sequences are selected. The polypeptides or nucleic acids encoding them
XX CC are useful for identifying modulators. The identified modulators are
XX CC useful as herbicides.
XX CC Sequence 502 AA;
XX SQ

Query Match 99.7%; Score 2607; DB 23; Length 502;
Best Local Similarity 99.8%; Pred. No. 7.9e-241;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 MVLHSAVSDSVHSTFASRYVTSLSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
Db 1 MVLHSAVSDSVHSTFASRYVTSLSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
Qy 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATAVG 120
Db 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATAVG 120
Qy 121 VGTGVSSEAIMLAGLAFKRWQKKAEGKPVDPKNIVTGANVQVCWEKFPARYFEVELKE 180
Db 121 VGTGVSSEAIMLAGLAFKRWQKKAEGKPVDPKNIVTGANVQVCWEKFPARYFEVELKE 180
Qy 181 VKLSEGYVMDPQAAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
Db 181 VKLSEGYVMDPQAAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
Qy 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKINSVGHKYLTVAGIWNKEDLPEEL 300
Db 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKINSVGHKYLTVAGIWNKEDLPEEL 300
Qy 301 IFHINYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNWNCNEMIVLREGLEK 360
Db 301 IFHINYLGADQPTFTLNFSGSSQVIAQYQIIRLGHGEGYNNWNCNEMIVLREGLEK 360
Qy 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHIITVLRV 420
Db 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIPAYTMPNQAQHIITVLRV 420
Qy 421 IREDFSRTLAERLVIDIEKVMRELDLPSPRVTHKISLGQEKSESNDLMVTVKKSDDIK 480
Db 421 IREDFSRTLAERLVIDIEKVMRELDLPSPRVTHKISLGQEKSESNDLMVTVKKSDDIK 480
Qy 481 QRDIIITGWKKFVADRKKTSGIC 502
Db 481 QRDIIITGWKKFVADRKKTSGIC 502

```

RESULT 3
D AAO15139 standard; Protein; 500 AA.
X
C AAO15139;
X
C 25-SEP-2002 (first entry)
X
C Petunia GAD protein.
X
C GAD; plant GABA production regulation; glutamic acid decarboxylase;
X
C plant stress; GABA; gamma-aminobutyric acid; stress resistance.
X
C Petunia sp.
X
C WO200238736-A2.
X
C 16-MAY-2002.
X
C 07-NOV-2001; 2001WO-US47447.
X
C 07-NOV-2000; 2000US-246367P.
X
C (EMER-) EMERALD BIOAGRICULTURE CORP.
X
C Kinnersley AM, Turano FJ;
X
C WPI; 2002-490073/52.
X
C N-PSDB; AAL43417.
X
C Making transformed plants that selectively increase gamma-aminobutyric
X
C acid production, by incorporating a DNA construct with a polynucleotide
X
C encoding a plant glutamic acid decarboxylase enzyme into plant's genome
X
C
X
C Claim 17; Page 58; 63pp; English.
X
C The present invention relates to a method of producing a transformed
X
C plant that selectively increases production of gamma-aminobutyric acid
X
C (GABA) in response to a signal, by incorporating into the plant's genome
X
C a DNA construct with a non-constitutive promoter operably linked to a
X
C polynucleotide encoding a functional plant glutamic acid decarboxylase
X
C (GAD), to provide a transformed plant that expresses the GAD coding
X
C sequence in response to a signal. Plants of this type have an enhanced
X
C ability to tolerate environmental or other stresses. The present sequence
X
C is the petunia GAD protein.
X
C
X
C Sequence 500 AA;
X
C
X
C Query Match 86.0%; Score 2250; DB 23; Length 500;
X
C Best Local Similarity 84.9%; Pred. No. 1.4e-206;
X
C Matches 427; Conservative 39; Mismatches 33; Indels 4; Gaps 2;
X
C
X
C 1 MVLSHAVSESDVSVHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDELMLDGNPRLNL 60
X
C 1 MVLKSTVQSQSDVSIHSTFASRYVRTSLPRFKMPDPSIPKEAAYQIINDELMLDGNPRLNL 60
X
C 61 ASFTVTWNEPCDKLISSINKNVDMDEYPTVTELQNCVNMIAHLFNAPLBEAETAVG 120
X
C 61 ASFTVTWNEPCDKLISSINKNVDMDEYPTVTELQNCVNMIAHLFNAPLBEAETAVG 120
X
C 121 VGTVGSSSAIMLAGLAFKRKQNKREKARGKPDVDPNIVTGANVQVCWEKFARYPEVELKE 180
X
C 121 VGTVGSSSAIMLAGLAFKRKQNKREKARGKPDVDPNIVTGANVQVCWEKFARYPEVELKE 180
X
C 181 VKLSEGYVMDPQQAVMDVENTICVADILGSTLNGEFEDVKLINDLLVEKNKETGMDTP 240
X
C 181 VKLSEGYVMDPERAVENMDVENTICVAILGSTLNGEFEDVKRLNDLLVEKNKETGMDTP 240
X
C 241 IHVDAASGGFIAPFIYPELEWDFRLPLVKSINVSGHKYGLVYAGIWNKRNKEDLPEEL 300
X
C 241 IHVDAASGGFIAPFIYPELEWDFRLPLVKSINVSGHKYGLVYAGIWNKRNKEDLPEEL 300
X
C
X
C RESULT 4
X
C AAO15137
X
C ID AAO15137 standard; Protein; 496 AA.
X
C AC AAO15137;
X
C DT 25-SEP-2002 (first entry)
X
C DE Tobacco GAD1.
X
C KW GAD; plant GABA production regulation; glutamic acid decarboxylase;
X
C KW plant stress; GABA; gamma-aminobutyric acid; stress resistance.
X
C OS Nicotiana tabacum.
X
C XX WO200238736-A2.
X
C PN 16-MAY-2002.
X
C PD 07-NOV-2001; 2001WO-US47447.
X
C PF 07-NOV-2000; 2000US-246367P.
X
C PR (EMER-) EMERALD BIOAGRICULTURE CORP.
X
C XX Kinnersley AM, Turano FJ;
X
C XX WPI; 2002-490073/52.
X
C DR N-PSDB; AAL43415.
X
C DR Making transformed plants that selectively increase gamma-aminobutyric
X
C acid production, by incorporating a DNA construct with a polynucleotide
X
C encoding a plant glutamic acid decarboxylase enzyme into plant's genome
X
C
X
C Claim 17; Page 57; 63pp; English.
X
C The present invention relates to a method of producing a transformed
X
C plant that selectively increases production of gamma-aminobutyric acid
X
C (GABA) in response to a signal, by incorporating into the plant's genome
X
C a DNA construct with a non-constitutive promoter operably linked to a
X
C polynucleotide encoding a functional plant glutamic acid decarboxylase
X
C (GAD), to provide a transformed plant that expresses the GAD coding
X
C sequence in response to a signal. Plants of this type have an enhanced
X
C ability to tolerate environmental or other stresses. The present sequence
X
C is the tobacco GAD1 protein.
X
C
X
C Sequence 496 AA;
X
C
X
C Query Match 85.7%; Score 2240; DB 23; Length 496;
X
C Best Local Similarity 85.1%; Pred. No. 1.2e-205;
X
C Matches 428; Conservative 35; Mismatches 32; Indels 8; Gaps 3;
X
C
X
C 1 MVLSHAVSESDVSVHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDELMLDGNPRLNL 60
X
C 1 MVLKSTASSEDVSIHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDELMLDGNPRLNL 60

```

61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEFTAVG 120
 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEFTAVG 120
 121 VGTGVSSEAIMLAGLAFKRWQKRAEGKPVDPKPNIVTGANVQVQWCKEPARYFEVELKE 180
 121 VGTGVSSEAIMLAGLAFKRWQKRAEGKPVDPKPNIVTGANVQVQWCKEPARYFEVELKE 180
 181 VKLSEGYVMDPOQAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
 181 VKLSDGYVMDPEKAVMVDENTICVAILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIOWAIVRNKEDLPDEL 300
 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIOWAIVRNKEDLPDEL 300
 301 IFHNYLGADQPTFTLNFSGSSQVIAQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 360
 301 IFHNYLGADQPTFTLNFSGSSQVIAQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 360
 361 TERFNIVSKDEGVPLVAFSLKDSCHTEPEISDMLRRYGVIPAYTMPNACHITVLRVV 420
 361 SGRFNIISKEIGVPLVAFSLKDSCHTEPEISDMLRRYGVIPAYTMPNACHITVLRVV 420
 421 IREDFRTLAERLVIDIEKVMRELDELPSRVHKSILGOEKSESNDMLVTVKSDIDK 480
 421 IREDFRTLAERLVIDIEKVMRELDELPSRVHKSILGOEKSESNDMLVTVKSDIDK 480
 481 ORDITITGWKKFVAD-RKKTSGIC 502
 474 QLEITTAWLKFWADKKKTNGVC 496

RESULT 5
 AAO15138 standard; Protein; 496 AA.
 AAO15138;
 25-SEP-2002 (first entry)
 Tobacco GAD2.
 GAD; plant GABA production regulation; glutamic acid decarboxylase;
 plant stress; GABA; gamma-aminobutyric acid; stress resistance.
 Nicotiana tabacum.
 WO200238736-A2.
 16-MAY-2002.
 07-NOV-2001; 2001WO-US47447.
 07-NOV-2000; 2000US-246367P.
 (EMER-) EMERALD BIOAGRICULTURE CORP.
 Kinnersley AM, Turano FJ;
 WPI; 2002-490073/52.
 N-FSDB; AAL43416.
 Making transformed plants that selectively increase gamma-aminobutyric
 acid production, by incorporating a DNA construct with a polynucleotide
 encoding a plant glutamic acid decarboxylase enzyme into plant's genome
 Claim 17; Page 58; 63pp; English.
 The present invention relates to a method of producing a transformed
 plant that selectively increases production of gamma-aminobutyric acid

CC (GABA) in response to a signal, by incorporating into the plant's genome
 a DNA construct with a non-constitutive promoter operably linked to a
 polynucleotide encoding a functional plant glutamic acid decarboxylase
 (GAD), to provide a transformed plant that expresses the GAD coding
 sequence in response to a signal. Plants of this type have an enhanced
 ability to tolerate environmental or other stresses. The present sequence
 is the tobacco GAD2 protein.
 XX Sequence 496 AA;
 SQ
 Query Match 84.1%; Score 2199; DB 23; Length 496;
 Best Local Similarity 84.1%; Pred. No. 1.1e-201;
 Matches 423; Conservative 34; Mismatches 38; Indels 8; Gaps 3;
 QY 1 MVLHAVSESQVSHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDELMLDGNPRLN 60
 DB 1 MVLKTAQSDSVSHSTFASRYVRTSLPRFKMPENSIPKEAAYQIINDELMLDGNPRLN 60
 QY 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEFTAVG 120
 DB 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTTELQNRQVNMIAHLFNAPLEAEFTAVG 120
 QY 121 VGTGVSSEAIMLAGLAFKRWQKRAEGKPVDPKPNIVTGANVQVQWCKEPARYFEVELKE 180
 DB 121 VGTGVSSEAIMLAGLAFKRWQKRAEGKPVDPKPNIVTGANVQVQWCKEPARYFEVELKE 180
 QY 181 VKLSEGYVMDPOQAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
 DB 181 VKLSDGYVMDPEKAVMVDENTICVAILGSTLNGEFEDVKLLNDLLVEKNKKTGWDTP 240
 QY 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIOWAIVRNKEDLPDEL 300
 DB 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIOWAIVRNKEDLPDEL 300
 QY 301 IFHNYLGADQPTFTLNFSGSSQVIAQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 360
 DB 301 IFHNYLGADQPTFTLNFSGSSQVIAQYQYQYQYQYQYQYQYQYQYQYQYQYQYQYQY 360
 QY 361 TERFNIVSKDEGVPLVAFSLKDSCHTEPEISDMLRRYGVIPAYTMPNACHITVLRVV 420
 DB 361 SGRFNIISKEIGVPLVAFSLKDSCHTEPEISDMLRRYGVIPAYTMPNACHITVLRVV 420
 QY 421 IREDFRTLAERLVIDIEKVMRELDELPSRVHKSILGOEKSESNDMLVTVKSDIDK 480
 DB 421 IREDFRTLAERLVIDIEKVMRELDELPSRVHKSILGOEKSESNDMLVTVKSDIDK 480
 QY 481 ORDITITGWKKFVAD-RKKTSGIC 502
 DB 474 QLEITTAWLKFWADKKKTNGVC 496

RESULT 6
 AAO15135
 ID AAO15135 standard; Protein; 493 AA.
 XX
 AC AAO15135;
 XX
 DT 25-SEP-2002 (first entry)
 XX
 DE A thaliana GAD4.
 XX
 KW GAD; plant GABA production regulation; glutamic acid decarboxylase;
 KW plant stress; GABA; gamma-aminobutyric acid; stress resistance.
 XX
 OS Arabidopsis thaliana.
 XX
 PN WO200238736-A2.
 XX
 PD 16-MAY-2002.
 XX
 PF 07-NOV-2001; 2001WO-US47447.
 XX
 PR 07-NOV-2000; 2000US-246367P.

(EMER-) EMERALD BIOAGRICULTURE CORP.

Kinnersley AM, Turano FJ;

WPI; 2002-490073/52.

N-ESDS; AAL43413.

Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome

Claim 17; Page 55-56; 63pp; English.

The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAD), to provide a transformed plant that expresses the GAD coding sequence in response to a signal. Plants of this type have an enhanced ability to tolerate environmental or other stresses. The present sequence is the A. thaliana GAD4 protein.

Sequence 493 AA;

```

Query Match      81.7%; Score 2135.5; DB 23; Length 493;
Best Local Similarity 82.4%; Pred. No. 1.3e-195;
Matches 411; Conservative 32; Mismatches 45; Indels 11; Gaps 2;

/ 1 MVLSHAVSESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
b 1 MVLKTVSESDVSHSTFASRYVRNSLPRFEMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
y 61 ASFTVTWMEPCDKLIMSSINKNVDMDEYVPTTELQNCVNMIAHFNAPLEEAFTAVG 120
b 61 ASFTVTWMEPCDKLIMESINKNVDMDEYVPTTELQNCVNMIAHFNAPLDGEEAVG 120
y 121 VGTGVSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIIVTGANVQVCWEKFARYFEVELKE 180
b 121 VGTGVSSEAIMLAGLAFKRWQNKRAEQGLPYDKPNIIVTGANVQVCWEKFARYFEVELKE 180
y 181 VKLSEGVYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKTCGWDTP 240
b 181 VNLREDYVMDPVKAVEMVDENTICVAAILGSTLTGFEFEDVKLLNDLLVEKNKTCGWDTP 240
y 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 360
b 301 IFHINYLGAQOPTFTLNFSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 360
y 361 TERFNIVSKDEGVLPAFSLKSDSCHTEFEISDMLRRYGVIPAYTMPNNAQHITVLRVV 420
b 361 TGRPKIVSKENGVPVLAFLSKDSRNEFEVAHTLRFGWIVPAYTMPADAAQHVTVLRVV 420
y 421 IHVDAASGGFTAPFLYPELEWDFRLPLVKSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 480
b 421 IREDPSRTLAERLVIDTKVMRELDLPSRVTHKISLGQKSESNSDNLMTVTKSDIDK 480
y 481 ORDIITGKKKXVADRKKT 499
b 471 QREVTAYWKLL-ETKTN 488

```

RESULT 7
 ABB91695
 ID ABB91695 standard; Protein; 493 AA.
 XX
 AC ABB91695;

```

XX 31-MAY-2002 (first entry)
XX Herbicidally active polypeptide SEQ ID NO 906.
XX Herbicidal; plant; agriculture; herbicide.
XX Arabidopsis thaliana.
XX WO200210210-A2.
XX 07-FEB-2002.
XX 28-AUG-2001; 2001WO-EP09892.
XX 28-AUG-2001; 2001WO-EP09892.
XX (FARB ) BAYER AG.
XX Tietjen K, Weidner M;
XX WPI; 2002-269010/31.
XX Identifying plant target proteins for herbicidally active compounds,
XX comprising aligning and comparing nucleic acid or amino acid sequences
XX from plant with nucleic acid or amino acid sequences from non-plant
XX organisms -
XX Claim 5; SEQ ID NO 906; 261pp + Sequence Listing; English.
XX The invention relates to identifying target proteins
XX (ABB9790-ABB94016) for herbicidally active compounds, comprising
XX aligning and comparing nucleic acid or amino acid sequences from plant
XX with nucleic acid or amino acid sequences from non-plant organisms using
XX suitable search parameters, where plant sequences having an E-value
XX greater by a factor of 3 than the E-value of most similar non-plant
XX sequences are selected. The polypeptides or nucleic acids encoding them
XX are useful for identifying modulators. The identified modulators are
XX useful as herbicides.
XX Sequence 493 AA;
XX Query Match      81.7%; Score 2135.5; DB 23; Length 493;
XX Best Local Similarity 82.4%; Pred. No. 1.3e-195;
XX Matches 411; Conservative 32; Mismatches 45; Indels 11; Gaps 2;
XX 1 MVLSHAVSESDVSHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
XX 1 MVLKTVSESDVSHSTFASRYVRNSLPRFEMPENSIPKEAAAYQIINDELMLDGNPRLNL 60
XX 61 ASFTVTWMEPCDKLIMSSINKNVDMDEYVPTTELQNCVNMIAHFNAPLEEAFTAVG 120
XX 61 ASFTVTWMEPCDKLIMESINKNVDMDEYVPTTELQNCVNMIAHFNAPLDGEEAVG 120
XX 121 VGTGVSSEAIMLAGLAFKRWQNKRAEGKVPDKPNIIVTGANVQVCWEKFARYFEVELKE 180
XX 121 VGTGVSSEAIMLAGLAFKRWQNKRAEQGLPYDKPNIIVTGANVQVCWEKFARYFEVELKE 180
XX 181 VKLSEGVYVMDPQAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKTCGWDTP 240
XX 181 VNLREDYVMDPVKAVEMVDENTICVAAILGSTLTGFEFEDVKLLNDLLVEKNKTCGWDTP 240
XX 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 360
XX 241 IHVDAASGGFTAPFLYPELEWDFRLPLVKSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 360
XX 301 IFHINYLGAQOPTFTLNFSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 360
XX 301 IFHINYLGAQOPTFTLNFSGSSQVIAQYQLIRLGHGVRNWMNCRENMIVLRGLEK 360
XX 361 TERFNIVSKDEGVLPAFSLKSDSCHTEFEISDMLRRYGVIPAYTMPNNAQHITVLRVV 420
XX 361 TGRPKIVSKENGVPVLAFLSKDSRNEFEVAHTLRFGWIVPAYTMPADAAQHVTVLRVV 420

```



```

Query Match      81.5%; Score 2130; DB 23; Length 494;
Best Local Similarity 80.2%; Pred. No. 4.4e-195;
Matches 404; Conservative 46; Mismatches 42; Indels 12; Gaps 3;

1 MVLSHAVSDSVSHSTFASRYVRTSLPRFKMPENSIKPEAAVQIINDELMLDGNPRNL 60
1 MVLTKAT-NDSEVCTMFCGRVVRTSLPKYIIGENSIPKDAAYQIIDELMLDGNPRNL 59
61 ASFTVTWMEPECDKIMSSINKNYVDMEYPTVTELRQNCVNMIAHLFNAPLEAEAVG 120
60 ASFTVTWMEPECDKIMSSINKNYVDMEYPTVTELRQNCVNMIAHLFNAPLEAEAVG 119
121 VGTVGSSEALMAGLAFKRWKQKKAEGKPYDKPNIVTGANVQVCWEKARYFEVELKE 180
120 VGTVGSSEALMAGLAFKRWKQKKAEGKPYDKPNIVTGANVQVCWEKARYFEVELKE 179
181 VKLSEGYVMDPQQAQVMDVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
180 VNLSEGYVMDPQKAAMVDENTICVAILGSTLNGEFEDVKRLNDLLVKKNEBTGNTP 239
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSGHYGLVYAGIWMVWRNKEDLPEEL 300
240 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSGHYGLVYAGIWMVWRRAEDLPEEL 299
301 IFHINYLGAQDFTFLNFSKSSQVIAQYQILRLGHEGYRNVMNCRENNIIVLREGLEK 360
300 IFHINYLGAQDFTFLNFSKSSQVIAQYQILRLGHEGYRNVMNCRENNIIVLREGLEK 359
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGWIVPAYTWPNAQHITVLRVV 420
360 TERFNIVSKDQGVVAVFLKDKHSHFNFEISEMLRRFGWIVPAYTWPADQAHITVLRVV 419
421 IREDPSRTLAERLVIDIEKVMRELDLPFRVHKISLGQSKSESNMMLVTYKSDIDK 480
420 IREDPSRTLAERLVIDIEKVMRELDLPFRVHKISLGQSKSESNMMLVTYKSDIDK 479
481 Q--RDIIITGKKFVADRKTSGIC 502
471 EILMEVIVGWRKPFVKKKKNGVC 494

RESULT 10
AAO15134
ID AAO15134 standard; Protein; 500 AA.
AC AAO15134;
XX XX
XX XX
XX 25-SEP-2002 (first entry)
XX A thaliana GAD3.
XX GAD; plant GABA production regulation; glutamic acid decarboxylase;
XX plant stress; GABA; gamma-aminobutyric acid; stress resistance.
XX Arabidopsis thaliana.
XX WO200238736-A2.
XX 16-MAY-2002.
XX 07-NOV-2001; 2001WO-US47447.
XX 07-NOV-2000; 2000US-246367P.
XX (EMER-) EMERALD BIOAGRICULTURE CORP.
XX Kinnersley AM, Turano FU;
XX WPI; 2002-490073/52.
XX DR N-PSDB; AAL43412.
XX OS Arabidopsis thaliana.
XX Making transformed plants that selectively increase gamma-aminobutyric
PT acid production, by incorporating a DNA construct with a polynucleotide
PT encoding a plant glutamic acid decarboxylase enzyme into plant's genome
XX
XX Claim 17; Page 55; 63pp; English.
XX The present invention relates to a method of producing a transformed
XX plant that selectively increases production of gamma-aminobutyric acid
XX (GABA) in response to a signal, by incorporating into the plant's genome
XX a DNA construct with a non-constitutive promoter operably linked to a
XX polynucleotide encoding a functional plant glutamic acid decarboxylase
XX (GAD), to provide a transformed plant that expresses the GAD coding
XX sequence in response to a signal. Plants of this type have an enhanced
XX ability to tolerate environmental or other stresses. The present sequence
XX is the A. thaliana GAD1 protein.
XX Sequence 500 AA;
XX
Query Match      79.5%; Score 2080; DB 23; Length 500;
Best Local Similarity 78.8%; Pred. No. 2.8e-190;
Matches 395; Conservative 44; Mismatches 52; Indels 10; Gaps 1;

1 MVLSHAVSDSVSHSTFASRYVRTSLPRFKMPENSIKPEAAVQIINDELMLDGNPRNL 60
1 MVLSEKTSKSDSIHSTFASRYVRNLSISFEIPKNSIPKEAAYQIINDELKFDGNPRNL 60
61 ASFTVTWMEPECDKIMSSINKNYVDMEYPTVTELRQNCVNMIAHLFNAPLEAEAVG 120
61 ASFTVTWMEPECDKIMSSINKNYVDMEYPTVTELRQNCVNMIAHLFNAPLEAEAVG 120
121 VGTVGSSEALMAGLAFKRWKQKKAEGKPYDKPNIVTGANVQVCWEKARYFEVELKE 180
121 VGTVGSSEALMAGLAFKRWKQKKAEGKPYDKPNIVTGANVQVCWEKARYFEVELKE 180
181 VKLSEGYVMDPQQAQVMDVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
181 VKLSEGYVMDPQKAAMVDENTICVAILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSGHYGLVYAGIWMVWRNKEDLPEEL 300
241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSGHYGLVYAGIWMVWRNKEDLPEEL 300
301 IFHINYLGAQDFTFLNFSKSSQVIAQYQILRLGHEGYRNVMNCRENNIIVLREGLEK 360
301 IFHINYLGAQDFTFLNFSKSSQVIAQYQILRLGHEGYRNVMNCRENNIIVLREGLEK 360
361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGWIVPAYTWPNAQHITVLRVV 420
361 TERFNIVSKENGVPVPLVAFSLKDSCHTEFEISDMRLRYGWIVPAYTWPNAQHITVLRVV 420
421 IREDPSRTLAERLVIDIEKVMRELDLPFRVHKISLGQSKSESNMMLVTYKSDIDK 480
421 IREDPSRTLAERLVIDIEKVMRELDLPFRVHKISLGQSKSESNMMLVTYKSDIDK 479
481 QDIIITGKKFVADRKTSGI 501
471 CREVTAYWKKFVDTKDKNGV 491

RESULT 11
ABB91694
ID ABB91694 standard; Protein; 500 AA.
XX XX
XX AC ABB91694;
XX XX
XX 31-MAY-2002 (first entry)
XX Herbicidally active polypeptide SEQ ID NO 905.
XX Herbicidal; plant; agriculture; herbicide.
XX Arabidopsis thaliana.
XX OS Arabidopsis thaliana.
XX XX

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WO200210210-A2.

07-FEB-2002.

28-AUG-2001; 2001WO-EP09892.

28-AUG-2001; 2001WO-EP09892.

(FARB) BAYER AG.

Tietjen K, Weidler M;

WPI; 2002-269010/31.

Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -

Claim 5; SEQ ID NO 905; 261pp + Sequence Listing; English.

The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.

Sequence 500 AA;

Query Match 79.5%; Score 2080; DB 23; Length 500;
Best Local Similarity 78.8%; Pred. No. 2.8e-190;
Matches 395; Conservative 44; Mismatches 52; Indels 10; Gaps 1;
1 MVLSHAVSESDVSHSTFASRYVTSIPRFKMPENSIPEKAAVQIINDELMGPNPLNL 60
1 MVLSTASKSDSDSIHSTFASRYVNSISRFEPKNSIPKEAAVQIINDELMGPNPLNL 60
61 ASFVTTWMEPCDKLIMSSINKNYVDMDYPTVTELQNRQVNMIAHLFNAPLEAEATAV 120
61 ASFVTTWMEPCDKLIMSSINKNYVDMDYPTVTELQNRQVNMIAHLFNAPLEAEATAV 120
121 VGTGSSSEAIMLAGLAFKRWQNRKKAEGKVPDKPNIVTGANVQVCWEKFARYFEVELK 180
121 VGTGSSSEAVMLAGLAFKRWQNRKKAEGKVPDKPNIVTGANVQVCWEKFARYFEVELK 180
181 VKLSEGYVMDPQQAQVMDVNTTICVADILGSTLNGEFEDVKLNDLLVEKNKGTGMDT 240
181 VKLSEGYVMDPQQAQVMDVNTTICVADILGSTLNGEFEDVKLNDLLVEKNKGTGMDT 240
241 IHVDAASGGFTAPFLYDLEWDFRLPLVKSNVSGHKYGLVYAGVGVWIRKSKEDLPDE 300
241 IHVDAASGGFTAPFLYDLEWDFRLPLVKSNVSGHKYGLVYAGVGVWIRKSKEDLPDE 300
301 IFHNYLGADQPTFLNFSKSSQVIAQYQILRLGHEGVNVMNCKENNI VLRLEGLEK 360
301 IFHNYLGADQPTFLNFSKSSQVIAQYQILRLGHEGVNVMNCKENNI VLRLEGLEK 360
361 TERENIVSKDGVPLVAFSLKSDSCHTEFELSMLRYGVNVPAYTPMPAQAHTVLRV 420
361 TERENIVSKDGVPLVAFSLKSDSCHTEFELSMLRYGVNVPAYTPMPAQAHTVLRV 420
421 IREDFSRRLAERLVLDIEKVMRELDLPSRVYHVKISLGOEKSESNDLMVTVKKSIDK 480
421 IREDFSRRLAERLVLDIEKVMRELDLPSRVYHVKISLGOEKSESNDLMVTVKKSIDK 480
481 QRDIIITGWKXFVADKKTSGI 501
471 QREVTAYWKKFVDTKDNKV 491

RESULT 12

AAO15140

ID AAO15140 standard; Protein; 502 AA.

XX AAO15140;

XX 25-SEP-2002 (first entry)

XX Tomato GAD protein.

XX GAD; plant GABA production regulation; glutamic acid decarboxylase; plant stress; GABA; gamma-aminobutyric acid; stress resistance.

XX Lycopersicon esculentum.

XX WO200238736-A2.

XX 16-MAY-2002.

XX 07-NOV-2001; 2001WO-US47447.

XX 07-NOV-2000; 2000US-246367P.

XX (EMER-) EMERALD BIOAGRICULTURE CORP.

XX Kimmersley AM, Turano FJ;

XX WPI; 2002-490073/52.

XX N-PSDB; AAL43418.

XX Making transformed plants that selectively increase gamma-aminobutyric acid production, by incorporating a DNA construct with a polynucleotide encoding a plant glutamic acid decarboxylase enzyme into plant's genome

Claim 17; Page 59; 63pp; English.

The present invention relates to a method of producing a transformed plant that selectively increases production of gamma-aminobutyric acid (GABA) in response to a signal, by incorporating into the plant's genome a DNA construct with a non-constitutive promoter operably linked to a polynucleotide encoding a functional plant glutamic acid decarboxylase (GAD), to provide a transformed plant that expresses the GAD coding sequence in response to a signal. Plants of this type have an enhanced ability to tolerate environmental or other stresses. The present sequence is the tomato GAD protein.

Sequence 502 AA;

Query Match 77.0%; Score 2014; DB 23; Length 502;

Best Local Similarity 76.0%; Pred. No. 6e-184;

Matches 387; Conservative 53; Mismatches 55; Indels 14; Gaps 5;

QY 1 MVL-SHAVSESDVSHSTFASRYVTSIPRFKMPENSIPEKAAVQIINDELMGPNPLNL 59
Db 1 MVLTTTSIKDSSELSHCTFASRYVQSLPKFKNPKKMPKEAAVQIINDELMGPNPLNL 60
QY 60 LASFVTTWMEPCDKLIMSSINKNYVDMDYPTVTELQNRQVNMIAHLFNAPLEAEATAV 119
Db 61 LASFVTTWMEPCDKLIMSSINKNYVDMDYPTVTELQNRQVNMIAHLFNAPVGDDEATV 120
QY 120 GVGTGSSSEAIMLAGLAFKRWQNRKKAEGKVPDKPNIVTGANVQVCWEKFARYFEVELK 179
Db 121 GVGTGSSSEAIMLAGLAFKRWQNRKKAEGKVPDKPNIVTGANVQVCWEKFARYFEVELK 180
QY 180 EVKLSEGYVMDPQQAQVMDVNTTICVADILGSTLNGEFEDVKLNDLLVEKNKGTGMDT 239
Db 181 EVKLSEGYVMDPQQAQVMDVNTTICVADILGSTLNGEFEDVKLNDLLVEKNKGTGMDT 240
QY 240 PIHVDAASGGFTAPFLYDLEWDFRLPLVKSNVSGHKYGLVYAGVGVWIRKSKEDLPDE 299
Db 241 PIHVDAASGGFTAPFLYDLEWDFRLPLVKSNVSGHKYGLVYAGVGVWIRKSKEDLPDE 300

with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.

Sequence 494 AA;		
Query Match 75.3%; Score 1969; DB 23; Length 494;		
Best Local Similarity 75.2%; Pred. No. 1.2e-179;		
Matches 373; Conservative 56; Mismatches 61; Indels 6; Gaps 3;		
1	MVL	SHVSESDVSHSTFASRYRTSLPFXKPNPENSIPKEAYQIINDELMDGNPLNL 60
	1	MVLA-TNSDSEHLHSTFASRYVRAVPRFRPDCHMPADAAQVINDLMDGNPLNL 59
61	ASF	VTTWMEPECDKLIMSSINKNYVDMDEYPTVTTLQNRQVNMIAHLFNAPLEAEATVG 120
	60	ASFVTTWMEPECDKLIMDSVNKYVDMDEYPTVTTLQNRQVNMIAHLFNAPVGEAAIG 119
121	VGT	VGSSEATMLAGLAFKRWQNRKAEKGPVDKPNIVTGANVQVCEKFPARYPEVELKE 180
	120	CGTVGSSEATMLAGLAFKRWQNRKAEKGPVDKPNIVTGANVQVCEKFPARYPEVELKE 179
181	VKL	SEGYVMDPQAVMDVENTICVADILGSTLNGEFEDVKLLMDLLEKXKGTGWDTP 240
	180	VKLSSEGYVMDPAKAVEMVDENTICVAAILGSTLNGEFEDVKQLNDLLEKXKGTGWT 239
241	IHD	ASGGFIAPFLPELEWDFPLVKSINVSCHKYGLVYAGIWMVWANKEDLPEEL 300
	240	IHDVASGGFIAPFLPDLEWDFPLVKSINVSCHKYGLVYAGVWVWTKDDLPPEL 299
301	IFH	INYLGAQDPTFTLNFSGSSQVIAQYQIIRLGHGEGYRNVNCRNNMIVLRGELK 360
	300	VFINYLGAQDPTFTLNFSGSSQIIAQYQYFIRLGFEGYKINMNCMDNARRLEGIE 359
361	TER	FNVSKDEGVLVAFSLKSSCHTEFEISDMRLRRGWIVPAPVTPPNAOHITVLRV 420
	360	TGRFNVSKDIDGVLVAFSLKSSKHTVFEIASELRKFGWIIIPATMPADACHAVLRV 419
421	IRD	FSPRTLAERIVIDIEKVMRELDLPSRVIRHKISLGOEKSESNLNMVTVKKSIDK 480
	420	IREDFSRGLADRLITHIIQVLKEIQLPSRIAHLAA---AAAVSGDBDEVVKVTKAKMSL 475
481	ORD	IITGCKKFAVDRK 496
	476	E-DITKWKRLVEHR 490
RESULT 15		
AAG13764		
ID AAG13764 standard; Protein; 494 AA.		
AC AAG13764;		
XX		
XX		
D7 17-OCT-2000 (first entry)		
XX		
DE Arabidopsis thaliana protein fragment SEQ ID NO: 13378.		
XX		
KW Protein identification; signal transduction pathway; metabolic pathway;		
KW hybridisation assay; Genetic mapping; gene expression control; promoter;		
KW termination sequence.		
XX		
OS Arabidopsis thaliana.		
XX		
PN EP1033405-A2.		
XX		
PD 06-SEP-2000.		
XX		
PF 25-FEB-2000; 2000EP-0301439.		
XX		
25-FEB-1999; 99US-0121825.		
PR		

PR	05-MAR-1999;	99US-0123180.
PR	09-MAR-1999;	99US-0123548.
PR	23-MAR-1999;	99US-0125788.
PR	25-MAR-1999;	99US-0126264.
PR	29-MAR-1999;	99US-0126785.
PR	01-APR-1999;	99US-0127462.
PR	08-APR-1999;	99US-0128234.
PR	08-APR-1999;	99US-0128714.
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PR	14-MAY-1999;	99US-0134256.
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PR	14-MAY-1999;	99US-0134421.
PR	14-MAY-1999;	99US-0134370.
PR	18-MAY-1999;	99US-0134768.
PR	19-MAY-1999;	99US-0134941.
PR	20-MAY-1999;	99US-0135124.
PR	21-MAY-1999;	99US-0135353.
PR	24-MAY-1999;	99US-0135829.
PR	25-MAY-1999;	99US-0136021.
PR	25-MAY-1999;	99US-0136392.
PR	28-MAY-1999;	99US-0136782.
PR	01-JUN-1999;	99US-0137222.
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PR	08-JUN-1999;	99US-0138094.
PR	10-JUN-1999;	99US-0138540.
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PR	18-JUN-1999;	99US-0139492.
PR	18-JUN-1999;	99US-0139454.
PR	18-JUN-1999;	99US-0139455.
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PR	22-SEP-1999;	99US-0155139.			
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PR	04-OCT-1999;	99US-0157117.			
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DB	1	MVLA-TNSDSEHLHSTFASRYVRAVVRPKFMDHCHMKDAAYQVINDELMLDGNPRLNL 59	DB	1	MVLA-TNSDSEHLHSTFASRYVRAVVRPKFMDHCHMKDAAYQVINDELMLDGNPRLNL 59
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DB	60	ASEVTTWMEPCDKLIMDSVKNKYVMDDEYPTTELONRCVNMIAHFFHAPVGEDEAAIG 119	DB	60	ASEVTTWMEPCDKLIMDSVKNKYVMDDEYPTTELONRCVNMIAHFFHAPVGEDEAAIG 119
QY	121	VGTVGSSEAIMLAGLAFKRWKQKRAEGKPVDPKPNIVTGANVQVCWEKFARYFEVELKE 180	QY	121	VGTVGSSEAIMLAGLAFKRWKQKRAEGKPVDPKPNIVTGANVQVCWEKFARYFEVELKE 180
DB	120	CGTVGSSEAIMLAGLAFKRWKQKRAEQGLPIDKPNIVTGANVQVCWEKFARYFEVELKE 179	DB	120	CGTVGSSEAIMLAGLAFKRWKQKRAEQGLPIDKPNIVTGANVQVCWEKFARYFEVELKE 179
QY	181	VKLSEGYVMDPQOAVDMVDENTI CVADILGSLNGSEFEDVKLLNDLLVERKKEGTWDTP 240	QY	181	VKLSEGYVMDPQOAVDMVDENTI CVADILGSLNGSEFEDVKLLNDLLVERKKEGTWDTP 240
DB	180	VKLSEDIYYMDPAKAVEMVDENTICVAAILGSLTGEFEDVQLNDLLAEKKAETGWETP 239	DB	180	VKLSEDIYYMDPAKAVEMVDENTICVAAILGSLTGEFEDVQLNDLLAEKKAETGWETP 239
QY	241	IHVDAASGGFIAPFLYPELEWDFRPLVKSINVSCHKYGLVYAGIGWILWRNKBDLPEEL 300	QY	241	IHVDAASGGFIAPFLYPELEWDFRPLVKSINVSCHKYGLVYAGIGWILWRNKBDLPEEL 300
DB	240	IHVDAASGGFIAPFLYPDLLEWDFRPLVKSINVSCHKYGLVYAGVGNVWRKDDLPEEL 299	DB	240	IHVDAASGGFIAPFLYPDLLEWDFRPLVKSINVSCHKYGLVYAGVGNVWRKDDLPEEL 299
QY	301	IRHINYLGADQPTFTLNFSGSSQIAQYQYQIRLGHGEGYVNMENCRENMIVLREGLEK 360	QY	301	IRHINYLGADQPTFTLNFSGSSQIAQYQYQIRLGHGEGYVNMENCRENMIVLREGLEK 360
DB	300	VPHINYLGADQPTFTLNFSGSSQIIAQYQYQIRLGFEGYKMINEMDNARRLEGIEM 359	DB	300	VPHINYLGADQPTFTLNFSGSSQIIAQYQYQIRLGFEGYKMINEMDNARRLEGIEM 359
QY	361	TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIVPAYTMPNAQHIVLVVV 420	QY	361	TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMRLRYGVIVPAYTMPNAQHIVLVVV 420
DB	360	TGKFNTIVSKDIGVPLVAFSLKDSKSHVTPEIAESLRKFGWIIIPAYTMPADAQHIALRVV 419	DB	360	TGKFNTIVSKDIGVPLVAFSLKDSKSHVTPEIAESLRKFGWIIIPAYTMPADAQHIALRVV 419
QY	421	IREDFSRTLAERLVIDIEKVMRELDELPSRVTHKISLGOEKSESNSDMLMVTVKSDIDK 480	QY	421	IREDFSRTLAERLVIDIEKVMRELDELPSRVTHKISLGOEKSESNSDMLMVTVKSDIDK 480
DB	420	IREDFSRGLADRLITHIIQVLKEIEGLPSRIAHLAA----AAVSGDDEEVKVTAKMSL 475	DB	420	IREDFSRGLADRLITHIIQVLKEIEGLPSRIAHLAA----AAVSGDDEEVKVTAKMSL 475
QY	481	ORDIITGWKKFVADRK 496	QY	481	ORDIITGWKKFVADRK 496
DB	476	E-DITKYWKLVEHKE 490	DB	476	E-DITKYWKLVEHKE 490

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protein - protein search, using sw model

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Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : PIR 76:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2250	86.0	500	2 A48767	glutamate decarbox
2	2199	84.1	496	2 T01962	glutamate decarbox
3	2135.5	81.7	493	2 H84431	probable glutamate
4	2130	81.5	494	2 H96683	hypothetical prote
5	2080	79.5	500	2 G84431	probable glutamate
6	2014	77.0	502	2 S56177	probable glutamate
7	1318	50.4	514	2 JC7915	glutamate decarbox
8	1318	50.4	520	2 T49478	probable glutamate
9	1251.5	47.9	467	2 S75150	glutamate decarbox
10	1110	42.4	460	2 F70975	probable glutamate
11	1108	42.4	475	2 T36342	probable glutamate
12	1028	39.3	466	2 B86786	glutamate decarbox
13	1013	38.7	466	1 B43332	glutamate decarbox
14	1013	38.7	466	1 S24234	glutamate decarbox
15	1013	38.7	466	2 B90891	glutamate decarbox
16	1013	38.7	466	2 G85726	glutamate decarbox
17	1009	38.6	466	2 E91178	glutamate decarbox
18	1009	38.6	466	2 F86024	glutamate decarbox
19	983	36.8	467	2 AC1748	glutamate decarbox
20	955.5	36.5	462	2 AH1130	glutamate decarbox
21	953.5	36.5	467	2 AB1379	glutamate decarbox
22	948	36.3	464	2 AB1740	glutamate decarbox
23	940	35.9	464	2 AC1370	glutamate decarbox
24	887.5	33.9	585	2 S53072	glutamate decarbox
25	635.5	24.3	304	2 AE3623	glutamate decarbox
26	335.5	12.8	167	2 AF3623	glutamate decarbox
27	325	12.4	589	2 S70123	spingosine-1-phos
28	314	12.0	384	2 G75102	group II decarboxy
29	312	11.9	363	2 E69015	glutamate decarbox

30 311 11.9 367 2 C69500 group II decarboxy
31 305 11.7 383 2 D71084 hypothetical prote
32 288 11.0 552 2 T33760 sphingosine-1-phos
33 270 10.3 544 2 C86405 probable sphingos
34 269.5 10.3 488 2 B69415 group II decarboxy
35 264.5 10.1 542 2 T29835 sphingosine-1-phos
36 249.5 9.5 355 2 D84192 glutamate decarbox
37 246.5 9.4 568 2 JC5923 glutamate decarbox
38 243.5 9.3 473 2 G72753 hypothetical prote
39 225 8.6 396 2 B64306 hypothetical prote
40 206.5 7.9 414 2 G69536 group II decarboxy
41 203 7.8 454 2 G72452 probable glutamate
42 147 5.6 557 2 F82481 decarboxylase, gro
43 144.5 5.5 548 2 H82234 probable glutamate
44 142.5 5.4 482 2 E96500 probable histidine
45 137 5.2 413 1 S39554 histidine decarbox

RESULT 1
A48767
glutamate decarboxylase (EC 4.1.1.15), calmodulin-binding - garden petunia
C/Species: Petunia x hybrida (garden petunia)
C/Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 22-Jun-1999
C/Accession: A48767
R/Baum, G.; Chen, Y.; Azazi, T.; Takatsuji, H.; Fromm, H.
J. Biol. Chem. 268, 19610-19617, 1993
A/Title: A plant glutamate decarboxylase containing a calmodulin binding domain. Cloning
A/Reference number: A48767; MUID:93374956; PMID:8366104
A/Accession: A48767
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-500 <BAU>
A/Cross-references: GB:L16797; NID:G294111; PIDN:AAA33709.1; PID:G294112
C/Superfamily: Escherichia coli glutamate decarboxylase
C/Keywords: calmodulin binding; carbon-carbon lyase; carboxy-lyase

Query Match 86.0%; Score 2250; DB 2; Length 500;
Best Local Similarity 84.9%; Pred. No. 1.5e-150;
Matches 427; Conservative 39; Mismatches 33; Indels 4; Gaps 2;

Qy 1 MVLGSHVSESDVSVHSTFASRYVTSLSLPRFKMPENSIPEAAAYQIINDELMLDGNRLNL 60
Db 1 MVLGSHVSESDVSVHSTFASRYVTSLSLPRFKMPENSIPEAAAYQIINDELMLDGNRLNL 60
Qy 61 ASFTVTWMEPECDKLIMSSINKNYVDMEYPTVTELRQNCVNMIAHLENAPLEAEATAVG 120
Db 61 ASFTVTWMEPECDKLIMSSINKNYVDMEYPTVTELRQNCVNMIAHLENAPLEAEATAVG 120
Qy 121 VGTGSSSEATMLAGLAFKRWQNKRAEGKVPDKPNIVTGANYQVCWEKFPARYFEVELKE 180
Db 121 VGTGSSSEATMLAGLAFKRWQNKRAEGKVPDKPNIVTGANYQVCWEKFPARYFEVELKE 180
Qy 181 VKLSEGYVNDPQAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
Db 181 VKLSEGYVNDPQAVDMVDENTICVADILGSTLNGEFEDVKLLNDLLVEKNKETGWDTP 240
Qy 241 IHVDAASGGFIAPFLYPELEWDPRFLPVKSINVSCHKYGLVYAGIGWTVRNKEDLPEEL 300
Db 241 IHVDAASGGFIAPFLYPELEWDPRFLPVKSINVSCHKYGLVYAGIGWTVRNKEDLPEEL 300
Qy 301 IFHNYLGADQPTFTLNFSKSSQVIAQYQLIRLGHGYNVNMENCRNINVLREGLEK 360
Db 301 IFHNYLGADQPTFTLNFSKSSQVIAQYQLIRLGHGYNVNMENCRNINVLREGLEK 360
Qy 361 TERPNIVSKDEGVPLVAPSLKDSCHTEFEISMLRRYGWIIVPAYTPPNAQHITVLRVV 420
Db 361 TGRPNITSKIGVPLVAFSLKDRNQHNEFEISLTRRRFGWIVPAYTPPNAQHITVLRVV 420
Qy 421 IREDFSRTLAERLVIDIEKVMRELDELPSRVHKSISLGQKSESNDMLMVTVKKSDIDK 480

ALIGNMENTS

b 421 IREDFSRITLAERLVRIEDIEKVLHELOTLPARVNAKLAVAEQAAANGSEVH---KKITDSEV 477
y 481 QRDITIGWKFFVAD-RKKTSGIC 502
b 478 QLEMITAWLKFVEEKKKTNKRV 500

RESULT 2
01962
lutamate decarboxylase (EC 4.1.1.15) 2, calmodulin-binding - common tobacco
,Species: Nicotiana tabacum (common tobacco)
,Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Jun-1999
,Accession: T01962
,Yun, S.J.; Oh, S.H.
,Cells 8, 125-129, 1998
,Title: Cloning and characterization of a tobacco cDNA encoding calcium/calmodulin-depe
,Reference number: Z14473; MUID:98302498; PMID:9638642
,Accession: T01962
,Status: preliminary; translated from GB/EMBL/DBJ
,Molecule type: mRNA
,Residues: 1-496 <YUN>
Cross-references: EMBL:AF020424; NID:g3252853; PIDN:AAC39483.1; PID:g3252854
Genetics:
Gene: GAD2
Function:
Description: catalyzes the formation of gamma-aminobutyric acid, from L-glutamic acid
Superfamily: Escherichia coli glutamate decarboxylase
Keywords: calmodulin binding; carbon-carbon lyase; carboxy-lyase

Query Match 84.1%; Score 2159; DB 2; Length 496;
Best Local Similarity 84.1%; Pred. No. 5.8e-147;
Matches 423; Conservative 34; Mismatches 38; Indels 8; Gaps 3;

/ 1 MVLHSAVSDSVHSTFASRYVRTSLPRFKNPENSIKPEAAAYQIINDELMIDGNPRLNL 60
> 1 MVLKTSASDVSVDHSTFASRYVRTSLPRFKNPENSIKPEAAAYQIINDELMIDGNPRLNL 60
/ 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATVG 120
> 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATVG 120
/ 121 VGTGSGSEAIMLAGLAFKRWQKKAQGLPYDKNIVTGANVQVCWEKFPARYFEVLEKE 180
/ 121 VGTGSGSEAIMLAGLAFKRWQKKAQGLPYDKNIVTGANVQVCWEKFPARYFEVLEKE 180
/ 181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEPEDVKLLNDLLVERKNETGWDTP 240
/ 181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEPEDVKLLNDLLVERKNETGWDTP 240
/ 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWIVWRNKEDLPBEL 300
/ 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWIVWRNKEDLPBEL 300
/ 301 IFHINYLGDQPTFTLNFSGSSQVIAQYQIIRLGHEGYRNVMENCRNMIVLREGLEK 360
/ 301 IFHINYLGDQPTFTLNFSGSSQVIAQYQIIRLGHEGYRNVMENCRNMIVLREGLEK 360
/ 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMPNQAQHTVLRV 420
/ 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMPNQAQHTVLRV 420
/ 421 IREDFSRITLAERLVRIEDIEKVMRLDPSRVTHKISLGQEKSESNMIVTVKSDIDK 480
/ 421 IREDFSRITLAERLVRIEDIEKVMRLDPSRVTHKISLGQEKSESNMIVTVKSDIDK 480
/ 481 QRDITIGWKFFVAD-RKKTSGIC 502
/ 478 QLEMITAWLKFVEEKKKTNKRV 500

SULT 3
4431
obable glutamate decarboxylase [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: H84431
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84431
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-493 <STO>
A;Cross-references: GB:AE002093; NID:g4406789; PIDN:AAD20099.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g02010
A;Map position: 2
C;Superfamily: Escherichia coli glutamate decarboxylase

Query Match 81.7%; Score 2135.5; DB 2; Length 493;
Best Local Similarity 82.4%; Pred. No. 1.7e-142;
Matches 411; Conservative 32; Mismatches 45; Indels 11; Gaps 2;

Qy 1 MVLHSAVSDSVHSTFASRYVRTSLPRFKNPENSIKPEAAAYQIINDELMIDGNPRLNL 60
Db 1 MVLKTSVSSDVSISHTFASRYVRNLSLPRFNPENSIKPEAAAYQIINDELMIDGNPRLNL 60
Qy 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATVG 120
Db 61 ASFTVTWMEPCDKLIMSSINKNYVDMDEYPTVTELQNCVNMIAHLFNAPLEAEATVG 120
Qy 121 VGTGSGSEAIMLAGLAFKRWQKKAQGLPYDKNIVTGANVQVCWEKFPARYFEVLEKE 180
Db 121 VGTGSGSEAIMLAGLAFKRWQKKAQGLPYDKNIVTGANVQVCWEKFPARYFEVLEKE 180
Qy 181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEPEDVKLLNDLLVERKNETGWDTP 240
Db 181 VKLSDGYVMDPEKAVEMVDENTICVAAILGSTLNGEPEDVKLLNDLLVERKNETGWDTP 240
Qy 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWIVWRNKEDLPBEL 300
Db 241 IHVDAASGGFIAPFLYPELEWDFRLPLVKSINVSCHKYGLVYAGIGWIVWRNKEDLPBEL 300
Qy 301 IFHINYLGDQPTFTLNFSGSSQVIAQYQIIRLGHEGYRNVMENCRNMIVLREGLEK 360
Db 301 IFHINYLGDQPTFTLNFSGSSQVIAQYQIIRLGHEGYRNVMENCRNMIVLREGLEK 360
Qy 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMPNQAQHTVLRV 420
Db 361 TERFNIVSKDEGVPLVAFSLKDSCHTEFEISDMLRRYGVIVPAYTMPNQAQHTVLRV 420
Qy 421 IREDFSRITLAERLVRIEDIEKVMRLDPSRVTHKISLGQEKSESNMIVTVKSDIDK 480
Db 421 IREDFSRITLAERLVRIEDIEKVMRLDPSRVTHKISLGQEKSESNMIVTVKSDIDK 480
Qy 481 QRDITIGWKFFVAD-RKKTSGIC 499
Db 471 QREVTAYWKKLL-ETAKTN 488

RESULT 4
H96683
hypotheical protein F12P19.12 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: H96683
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.


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aps 1;
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AAIG 120
ELKE 180

ELKE 180
WDTP 240

WDTP	240
PEEL	300

PDEL 300
GLEK 360

GLEK 360
LRVV 420

LRVV 420
DIDK 480

PEET 470

1999

the character

55

aps 5;

||||| PRLN 60
ETAV 119

120 GYGTGSSBAIMLAGLAFKRWKQKKAEGKPVDPKNI VTGANVQVCWEKFAFYFEVELK 179
121 GYGTGSSBAIMLAGLAFKRWKQKKAEGKPDKPNIVTGANVQVCWEKFAFYFEVELK 180
180 EVKLSGGYVMDPQAVMDVENTICVADILGSTLNGEFEDVKLLNDLLVEKNKGTGMDT 239
181 EVKLSGGYVMDPAKAVEIVDENTICVAAIIGSLTGTGEPEDVKLLNELLTKNKGWET 240
240 PIHVDAASGGFIAPFLYPLELWDFRLPLVKSINVSCHKYGLVYAGIAGVIVWENKEDLPEE 299
241 PIHVDAASGGFIAPFLWDFRLPLVKSINVSCHKYGLVYAGVGVIMWKSDELDE 300
300 LIPIHNYLGADQPTFTLNFSKGSSQVIAQYQILRLGHEGYRNVMENCRNMIVLREGLE 359
301 LVFIHNYLGSDQPTFTLNFSKGSYQIIAQYQILRLGFGYKNVKNCLSNKNAKVLTEGIT 360
360 KTERFNVSKDEGVPIVARSKDSCHTEFEISDMLRRYGVIVPAYTTPPNAQHITVLVRV 419
361 KMGRFDIVSKDVGVPVAFSLRDSKSYTVFEVSEHLRFGWIVPAYTTPPDAEHTAVLRV 420
420 VIREDFSRITLAERLVIDIEKWRELDPSRVTHKI--SLGQEKSESNDNL---WVTV 473
421 VIREDFSHSLAERLNSDIKILSELDTQPRPTKAVRVTAEEVRDDKGDGLHFFHMDTV 480
474 KKSIDIKQDRIIFGWKFFVADRKKTSIGIC 502
481 -----ETQKDIHKWRKIAG--KKTSGVC 502

RESULT 7

lutamate decarboxylase (EC 4.1.1.15) - Aspergillus oryzae
Species: Aspergillus oryzae
Date: 31-Mar-2003 #sequence_revision 31-Mar-2003 #text_change 21-Apr-2003
Accession: JG7915
Kato, Y.; Kato, Y.; Furukawa, K., and Hara, S.
J. Biosci. Biotechnol. Biochem. 66, 2600-2605, 2002
Title: Cloning and nucleotide sequence of the glutamate decarboxylase-encoding gene ga
Reference number: JG7915; MUID:22494577; PMID:12596854
Accession: JG7915
Molecule type: DNA
Residues: 1-514 <KAT>
Cross-references: DDBJ:AB025422
Comment: This enzyme produces gamma-aminobutyric acid.
Gene: gada
Introns: 79/2; 88/3; 477/2
Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 50.4%; Score 1318; DB 2; Length 514;
Best Local Similarity 56.8%; Pred. No. 6e-85;
Matches 256; Conservative 77; Mismatches 109; Indels 10; Gaps 5;
8 SESDVSVHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNLASFVTTW 67
28 TDEGYSVSSVGTFRATEQLPQEMPEREMPREVAVRMKDELSDGNPMLNLASFVTTI 87
68 MEPECDKLIMSSINKNVYMDYPTVTELRQNCVNMIAHLFNAPL--EAEATAVGVGTGVS 126
88 MEDEAEKLMTESLPKFNIDYEEYPOQAEIQNRCSVMIGRLFNAPVKAEDHPEMGSTIGS 147
127 SEAIMLAGLAFKRWKQKKAEGKPVDPKNI VTGANVQVCWEKFAFYFEVELKLSHG 186
148 SEAIMLGTLMARKRWKQKKAEGKYSRPNVMSAVQVCWEKATRYFEVEKFTVCTP 207
187 YYVMDPQAVMDVENTICVADILGSTLNGEFEDVKLLNDLLVEKNKGTGMDTPIHVDA 246
208 RYVIDPQAVDLVDENTIGICAILGTYTGYEDVKAINDLIERN----IDVPIHVDA 263
247 SGGFIAFLYPLELWDFRLPLVKSINVSCHKYGLVYAGIAGVIVWENKEDLPEELIFHNY 306
264 SGGFVAPFIPKLEWDFRLPKVVSINVSCHKYGLVYPGVGVVWRSPEYLPKDLIFNIN 323

307 LGADQPTFTLNFSKGSSQVIAQYQILRLGHEGYRNVMENCRNMIVLREGLEKTERFNI 366
324 LGAEQASFTLNFSKGASQVIGQYQIMIRLQKGRYSININIVTADFLAQELEKM-GFII 382
367 VS--KDEGVPLVAFSL--KDSSCHTEFEISDMLRRYGVIVPAYTTPPNAQHITVLRVIR 422
383 MSQRGHGLPLVAFRLPAEREGQDFBALAHQLRERGWIVPAYTMAPNSNNLKLMEVVVR 442
423 EDFSRITLAERLVIDIEKWRELDPSRVTHK 454
443 EDFTKSRCDALLSDIKLGUKTUGMDKAMDK 474
RESULT 8
T49478
probable glutamate decarboxylase [imported] - Neurospora crassa
N;Alternate names: protein B14D6.300
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Sep-2000
C;Accession: T49478
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Nyakatura,
submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49478
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-520 <SCH>
A;Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.300
A;Experimental source: BAC clone B14D6; strain OR74A
C;Genetics:
A;Gene: NCSP:B14D6.300
A;Map position: 6
A;Introns: 85/2; 504/3
C;Superfamily: Escherichia coli glutamate decarboxylase

Query Match 50.4%; Score 1318; DB 2; Length 520;
Best Local Similarity 55.6%; Pred. No. 6.1e-85;
Matches 262; Conservative 73; Mismatches 118; Indels 18; Gaps 6;
8 SESDVSVHSTFASRYVRTSLPRFKMPENSIPKEAAAYQIINDELMLDGNPRLNLASFVTTW 67
34 NDEDRFTTSYVSGKFAAADLPRHEMPDEMPKVAVMKDELSDGNPMLNLASFVTTI 93
68 MEPECDKLIMSSINKNVYMDYPTVTELRQNCVNMIAHLFNAPL--EAE--TAVGVGTG 125
94 MEDEAEKLMTESLPKFNIDYEEYPOQAEIQNRCSVMIGRLFNAPVKAEDASSAVGTSVG 153
126 SSEAIMLAGLAFKRWKQKKAEGKPVDPKNI VTGANVQVCWEKFAFYFEVELKLS 185
154 SSEAIMLGLVLMARKRWKQKKAEGKPADKPNLINSVAVQVCWEKATRYFEVEKFTVCTP 213
186 GYYVMDPQAVMDVENTICVADILGSTLNGEFEDVKLLNDLLVEKNKGTGMDTPIHVDA 245
214 DRYVIDPKETVDLVVENTIGICILGTYTGYEDVKAINDLVER---GLDTPIHVDA 269
246 ASGFIAPFLYPLELWDFRLPLVKSINVSCHKYGLVYAGIAGVIVWENKEDLPEELIFHIN 305
270 ASGGFVAPFVVPDLEWDFRLKNVVSINVSCHKYGLVYPGVGVVWRSAEYLPOELVFEN 329
306 YLGADQPTFTLNFSKGSSQVIAQYQILRLGHEGYRNVMENCRNMIVLREGLEKTERFN 365
330 YLGADQASFTLNFSKGASQVIGQYQILRLGKHGYRIMSNLTRTADYLAESLAAL-GFI 388
366 IVSK--DEGVPLVAFSLKDSCHT--EFEISDMLRRYGVIVPAYTTPPNAQHITVLRVVI 421
389 IMSKSGQGLPLVAFRLKEDPDRTYDEBALAHQLRERGWIVPAYTMAPKTEGLKMLRIV 448
422 REDESRTLAERLVIDI-----EKWRELDPSRVTHKISLGQEKSESN 465
449 REDFSNRCDGLSIDIRKSCQIGLEQMDKETVKKQBFHKKHVVVSGKASHN 499

[illegible]

b 40 PAHRLPDSPLPPESAYRLVHDELMLDGNARLNLAFTVTTWMEPQAGVLMSSECRDKNMIDK 99
y 88 DEYPTVTELQNRQVNMIAHLFNAPLEAEATAVGCTVGSSEAIMLAGLAFKEM--QNK 145
b 100 DEYPTAELELRCCVAMLAJLWHP--DPSTAVGCSVTGSSSEACMLAGALKRWRALRNAD 157
y 146 KARGKPDVDKNITGANVQVCEKFPARYFEVELKEVKLSEGYVMDPQOAVMDVDENTIC 205
b 158 RYPAKDV-RENLVGVNVQVCDKFCNFWEARQVPMESGDRFHLDPQAAAEELCDENIIG 216
y 206 VADILGSTINGEPEDVKLLNDLLVEKNKKTGMDTPHVDAAAGGFIAPIFLYPELWDPRLL 265
b 217 VVGLGSTFDGSEYEPADLCAALDALQERTGLDPVPHVDGASGAVAPFLDRLDVLMDPR 276
y 266 PLVKSINVSGHKYGLVYAGVIGWIKNKEDLPBELIFHINYLGAOQPTFLNFSKGSQV 325
b 277 PRVASINTSGHKYGLVYGVGVALWDAALPELVFRVNYLGGDMPTFALNFSRPAQV 336
y 326 IAQYQILRLGHGYNVNMENCNMIVREGLEKTERENIVSKDEGVPLVAFSLKDS-S 384
b 337 VAQYNFLRLGREGYRAVQQSARDIAGSLAERVAALGDFRLLTRGQDLPVFAFTTADVT 396
y 385 CHTEFEESDMLRYGVTPAYTTPPNAQHTVLRVVIREDPFRSLAERLVIDIEKVMREL 444
c 397 AYDVEDVRRRLRGGWLVPAITFPFPHREDLSVLRVVCRNGFSADWADLALLDLRLPEL 456
y 445 DELP 448
b 457 RRQP 460

RESULT 12
86786
lutamate decarboxylase (EC 4.1.1.15) [imported] - Lactococcus lactis subsp. lactis (str
, Species: Lactococcus lactis subsp. lactis
, Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
, Accession: B86786
, Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
genome Res. 11, 731-753, 2001
, Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
, Reference number: A86625; MUID:21235186; PMID:11337471
, Accession: B86786
, Status: preliminary
Molecule type: DNA
Residues: 1-466 <STO>
Cross-references: GB:AE005176; PID:g12724267; PIDN:AAK05388.1; GSPDB:GN00146
Experimental source: strain IL1403
Genetics:
Gene: gadB
Superfamily: Escherichia coli glutamate decarboxylase
Keywords: carbon-carbon lyase; carboxy-lyase

Query Match 39.3%; Score 1028; DB 2; Length 466;
Best Local Similarity 45.0%; Pred. No. 1.3e-64;
Matches 195; Conservative 91; Mismatches 141; Indels 6; Gaps 3;
/ 18 FASRYVTSIPLRFKPKPENSIPKEAAYQIINDELMDGNPRNLINASFVTTWMEPCDKLM 77
c 18 FGSSEQVDFPKYKLAQCSIEPRVAYQLVDMLDGNARLNLAFTVTTWMEPQAGVLMS 77
/ 78 SSINKNVYDMDYEPVTTTELQNRQVNMIAHLFNAPLEAEATAVGCTVGSSEAIMLAGLAF 137
c 78 QTLEKNAIDKSEYPTTEIENRCVNMIAHLWNA--SEKXFMGTSTIGSSSEACMLGMAW 135
/ 138 KRKQWKRKAEGKPDV--KNIVTGANVQVCEKFPARYFEVELKEVKLSEGYVMDPQQA 195
c 136 KFSWRKRAEKLGLDINAKPNLVISGQVCEKFCIYNDIENRVPMDKEHMSINLDKV 195
y 196 VDMVDENTICVADILGSTINGEPEDVKLLNDLLVEKNKKTGMDTPHVDAAAGGFIAPI 255
c 196 MDYVDYTIYGVVINGITGYTDYDIDKALNDLIEYNKQIDYKYIVHVDAAAGGLYAPFV 255
y 256 YPELWDPRLPVKSVINSGHKYGLVYAGVIGWIKNKEDLPBELIFHINYLGAOQPTFT 315

Db 256 EPELWDPRLPKWNISINTSGHKYGLVYGVGVLWDRKKYLPEELIPKVSYLGGELPTWA 315
Qy 316 LNFSGSSQVIAYQYQLIRLGHGYNVNMENCNMIVREGLEKTERENIVSKDEGVPL 375
Db 316 INFSSASQLIGYINFYRGFDGYKAIHERTHKVAFLAKEIEKTFGNFEIMNDGSQLPI 375
Qy 376 VAFSLDKDSCCH--TEFEISDMLRRYGVTPAYTTPPNAQHTVLRVVIREDPFRSLAERL 433
Db 376 VCYKLEKDSNRGNWLYDLADRLMLKMGQVPAYPLPKNLENEIQLRVIRADRCGNMAFY 435
Qy 434 VIDIEKVMRELD 446
Db 436 VDMQEAIEALNK 448

RESULT 13
B43332
glutamate decarboxylase (EC 4.1.1.15) beta - Escherichia coli (strain K-12)
N:Alternate names: L-glutamate 1-carboxy-lyase
C:Species: Escherichia coli
C:Date: 10-Mar-1994 #sequence_revision 23-Mar-1995 #text_change 01-Mar-2002
C:Accession: B43332; S30261; H64902
R:Smith, D.K.; Kassam, T.; Singh, B.; Elliott, J.F.
J. Bacteriol. 174, 5820-5826, 1992
A:Title: Escherichia coli has two homologous glutamate decarboxylase genes that map to
A:Reference number: A43332; MUID:92394884; PMID:1522060
A:Accession: B43332
A:Molecule type: DNA
A:Residues: 1-466 <SMI>
A:Cross-references: GB:M84025; NID:g146059; PIDN:AAA23834.1; PID:g146060
R:Yoshida, T.; Ueguchi, C.; Yamada, H.; Mizuro, T.
Mol. Gen. Genet. 237, 113-122, 1993
A:Title: Function of the Escherichia coli nucleoid protein, H-NS: molecular analysis of
A:Reference number: S30261; MUID:93204884; PMID:8455549
A:Accession: S30261
A:Molecule type: protein
A:Residues: 1-4, LQVL, 7-15 <YOS>
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: H64902
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-466 <BLAT>
A:Cross-references: GB:AE000246; GB:U00096; NID:g1787764; PIDN:AACT4566.1; PID:g1787769,
A:Experimental source: strain K-12, substrain MG1655
C:Genetics:
A:Gene: gadB
A:Map position: 78 min
A:Description:
C:Function:
A:Note: in E. coli, two isoforms (alpha and beta) have been found, each encoded by a sep
C:Superfamily: Escherichia coli glutamate decarboxylase
C:Keywords: carbon-carbon lyase; carboxy-lyase; homohexamer; phosphoprotein; pyridoxal
F:276/Binding site: pyridoxal phosphate (lys) (covalent) #status predicted

Query Match 38.7%; Score 1013; DB 1; Length 466;
Best Local Similarity 45.0%; Pred. No. 1.5e-63;
Matches 197; Conservative 83; Mismatches 152; Indels 6; Gaps 3;
Qy 16 STPASRVVTSIPLRFKPKPENSIPKEAAYQIINDELMDGNPRNLINASFVTTWMEPCDKL 75
Db 16 SRFGAKSISTIAESKRFPLHEMRDDVAQIINDELMDGNARQNLAFTQWDENVHKL 75
Qy 76 IMSSINKNVYDMDYEPVTTTELQNRQVNMIAHLFNAPLEAEATAVGCTVGSSEAIMLAGL 135
Db 76 MDLSINKNWIDKEYYPSAAILDLRCVNWADLWHPAPKNGQAVGNTIGSSSEACMLGGM 135
Qy 136 AFKRQWKRKAEGKPDVKNIVTGANVQVCEKFPARYFEVELKEVKLSEGYVMDPQQA 195

b 136 AMKWRWRKMEAAAGKPTDKPNLVCGP-VQICWHKFPARYWDVELRBPXRGQFLWMDPKRM 194
y 196 VDWVDENTTCVADILGSTLNGFEDVKLNDLLVKNKGTGHTDIHVDAASGGFIAPFL 255
b 195 IEACDENTTGWVTFGTGTYTGNVEFPQPLDHALDKFQADTGIDIMHDAASGGFLAPFV 254
y 256 YPELEWDFRLPLVKSINVSGHKYGLVYAGIGWVWRNKEDLPBELIFHINYLGAQDQFTT 315
b 255 APDIVWDFRLPRVKSISASGHKFLAPLGGWVWRNDEALQELVFNVDYLGQIGTGA 314
y 316 LNFSGKSSQVIAQYQILRLCHGYRNVMENCRNIVLRBGLKTERPNIV---SKDEG 372
b 315 INFSPAGQVIAQYEFRLGREGYTKVQNASVQVAAAYLADEBIAGLPGVEFTCTGRPDEG 374
y 373 VPLVAFSLKDS--CHTEFEISDMLRRYGVIPAYTMPNNAQHTVLRVWVIREDFSRTLA 430
b 375 IPAVCFKLKDGEDPGTYLDLSERLRLRGWQVPAFTLGGEATDIVVWRIMCRGFEMDFA 434
y 431 ERLVIDIEKVMRELDLP 448
o 435 ELLLEDYKASLKVLSDDHP 452

RESULT 14
24234
lutamate decarboxylase (EC 4.1.1.15) alpha - Escherichia coli (strain K-12)
, Alternate names: GAD alpha protein; L-Glutamate 1-carboxy-lyase
, Species: Escherichia coli
, Date: 22-Jan-1993 #sequence revision 05-Dec-1997 #text change 01-Mar-2002
, Accession: S47737; H65149; S24234; S2421; A43332; PN0616
, Plunkett, G.
submitted to the EMBL Data Library, March 1994
, Reference number: S47666
, Accession: S47737
, Status: preliminary
, Molecule type: DNA
, Residues: 1-466 <PLU>
, Cross-references: EMBL:U00039; NID:G466582; PIDN:AAB18493.1; PID:G466654
, Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
cience 277, 1453-1462, 1997
Title: The complete genome sequence of Escherichia coli K-12.
, Reference number: A64720; MUID:97426617; PMID:9278503
Accession: H65149
Status: nucleic acid sequence not shown; translation not shown
Molecule type: DNA
Residues: 1-466 <BLAT>
Cross-references: GB:AE000428; GB:U00096; NID:G1789931; PIDN:AACT6542.1; PID:G1789934;
Experimental source: strain K-12, substrain MG1655
Maras, B.; Sweeney, G.; Barra, D.; Bossa, F.; John, R.A.
ir, J. Biochem. 204, 93-98, 1992
Title: The amino acid sequence of glutamate decarboxylase from Escherichia coli. Evolu
Reference number: S23421; MUID:92155241; PMID:1740158
Accession: S24234
Molecule type: protein
Residues: 1-63 'S', 65-72 'R', 74-152 'N', 154-164 'S', 166-354 'N', 356-466 <MAR>
Accession: S23421
Molecule type: DNA
Residues: 148-164 'S', 166-207 'N', 209-294 'V', 296-431 <MAR1>
Cross-references: GB:X63123; NID:G41601; PIDN:CAA44834.1; PID:G938166
Smith, D.K.; Kassam, T.; Singh, B.; Elliott, J.F.
Bacteriol. 174, 5820-5826, 1992
Title: Escherichia coli has two homologous glutamate decarboxylase genes that map to d
, Reference number: A43332; MUID:92394884; PMID:1522060
Accession: A43332
Molecule type: DNA
Residues: 1-466 <SMI>
Cross-references: GB:M84024; NID:G146057; PIDN:AAA23833.1; PID:G146058
Note: sequence extracted from NCBI backbone (NCBIN:112979, NCBI:112980)
Yoshida, T.; Yamashino, T.; Ueguchi, C.; Mizuno, T.
losci. Biotechnol. Biochem. 57, 1568-1569, 1993
Title: Expression of the Escherichia coli dimorphic glutamic acid decarboxylases is re
Reference number: PN0616; MUID:94033862; PMID:7764225

A/Accession: PN0616
A/Molecule type: protein
A/Residues: 1-21, 'X' <YOS>
C/Genetics:
A/Gene: gacA
A/Map position: 78 min
C/Function:
A/Description: catalyzes the formation of gamma-aminobutyric acid, from L-glutamic acid
A/Note: in E. coli, two isoforms (alpha and beta) have been found, each encoded by a sep
C/Superfamily: Escherichia coli glutamate decarboxylase
C/Keywords: carbon-carbon lyase; carboxy-lyase; homohexamer; phosphoprotein; pyridoxal
F:2/6/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 38.7%; Score 1013; DB 1; Length 466;
Best Local Similarity 45.0%; Pred. No. 1.5e-63;
Matches 197; Conservative 83; Mismatches 152; Indels 6; Gaps 3;

Qy 16 STFASRVVTSLSRPRKMPENSIPKEAAQYQIINDELMDGNPRNLASFVTTWMEPCDKL 75
Db 16 SRFCAKAISTIAESKRPPLHEMRDDVAFQIINDELYLDGNARQNLATFCQTWDDENVHKL 75
Qy 76 IMGSINKNVVDMDBYPVTTBLQNKRCVNMIAHLNPALEBAETAVGVGTGVSSEALMAGL 135
Db 76 MDLSINKNWIDKSEYPOSAADILRCVNVVADLWEPAPKXGQAVGNTTIGSSEACHLGM 135
Qy 136 AFKKKQNKKAGKQVDPKNIVTGANVQVCKFPARYFEVELKEVKLSEGYVMDPQQA 195
Db 136 AMKWRWRKMEAAAGKPTDKPNLVCGP-VQICWHKFPARYWDVELRBPXRGQFLWMDPKRM 194
Qy 196 VDWVDENTTCVADILGSTLNGFEDVKLNDLLVKNKGTGHTDIHVDAASGGFIAPFL 255
Db 195 IEACDENTTGWVTFGTGTYTGNVEFPQPLDHALDKFQADTGIDIMHDAASGGFLAPFV 254
Qy 256 YPELEWDFRLPLVKSINVSGHKYGLVYAGIGWVWRNKEDLPBELIFHINYLGAQDQFTT 315
Db 255 APDIVWDFRLPRVKSISASGHKFLAPLGGWVWRNDEALQELVFNVDYLGQIGTGA 314
Qy 316 LNFSGKSSQVIAQYQILRLCHGYRNVMENCRNIVLRBGLKTERPNIV---SKDEG 372
Db 315 INFSPAGQVIAQYEFRLGREGYTKVQNASVQVAAAYLADEBIAGLPGVEFTCTGRPDEG 374
Qy 373 VPLVAFSLKDS--CHTEFEISDMLRRYGVIPAYTMPNNAQHTVLRVWVIREDFSRTLA 430
Db 375 IPAVCFKLKDGEDPGTYLDLSERLRLRGWQVPAFTLGGEATDIVVWRIMCRGFEMDFA 434
Qy 431 ERLVIDIEKVMRELDLP 448
Db 435 ELLLEDYKASLKVLSDDHP 452

RESULT 15
B90891
Glutamate decarboxylase isozyme [imported] - Escherichia coli (strain O157:H7, substrain
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C/Accession: B90891
R.Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: B90891
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-466 <HAY>
A/Cross-references: GB:BA000007; PIDN:BA035521.1; PID:G13361564; GSPDB:GN00154
A/Experimental source: strain O157:H7, substrain RMD 0509952
C/Genetics:
A/Gene: ECS2098
C/Superfamily: Escherichia coli glutamate decarboxylase

Query Match 38.7%; Score 1013; DB 2; Length 466;
Best Local Similarity 45.0%; Pred. No. 1.5e-63;

